

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:02:36 ; Search time 230 Seconds

(without alignments)
1208.601 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081

Sequence: 1 MEVNPMEGCGSGRPTTSF.....QELSNPLATLIPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1 | 2013 | 96.7 | 420 | 1 | GSK3B_HUMAN |
| 2 | 2013 | 96.7 | 420 | 1 | GSK3B_MOUSE |
| 3 | 2013 | 96.7 | 420 | 1 | GSK3B_HUMAN |
| 4 | 2013 | 96.7 | 420 | 1 | GSK3B_MOUSE |
| 5 | 2013 | 96.7 | 420 | 1 | GSK3B_MOUSE |
| 6 | 2006 | 96.4 | 420 | 2 | GSK3B_MOUSE |
| 7 | 1959 | 94.1 | 421 | 2 | GSK3B_MOUSE |
| 8 | 1959 | 94.1 | 421 | 2 | GSK3B_MOUSE |
| 9 | 1931 | 92.8 | 420 | 2 | GSK3B_MOUSE |
| 10 | 1931 | 92.8 | 420 | 2 | GSK3B_MOUSE |
| 11 | 1793.5 | 86.2 | 420 | 2 | GSK3B_MOUSE |
| 12 | 1704.5 | 81.9 | 440 | 2 | GSK3B_MOUSE |
| 13 | 1663.5 | 80.2 | 435 | 2 | GSK3B_MOUSE |
| 14 | 1663.5 | 80.1 | 407 | 2 | GSK3B_MOUSE |
| 15 | 1632 | 78.4 | 414 | 2 | GSK3B_MOUSE |
| 16 | 1614 | 77.6 | 414 | 2 | GSK3B_MOUSE |
| 17 | 1609 | 77.3 | 483 | 1 | GSK3A_HUMAN |
| 18 | 1607 | 77.2 | 483 | 1 | GSK3A_HUMAN |
| 19 | 1606 | 77.2 | 399 | 2 | GSK3B_MOUSE |
| 20 | 1594 | 76.6 | 388 | 2 | GSK3B_MOUSE |
| 21 | 1565 | 75.2 | 363 | 3 | GSK3B_MOUSE |
| 22 | 1542.5 | 74.1 | 1067 | 1 | GSK3B_MOUSE |
| 23 | 1495.5 | 71.9 | 443 | 2 | GSK3B_MOUSE |
| 24 | 1485 | 71.4 | 442 | 2 | GSK3B_MOUSE |
| 25 | 1443 | 69.3 | 431 | 2 | GSK3B_MOUSE |
| 26 | 1343.5 | 64.6 | 362 | 2 | GSK3B_MOUSE |
| 27 | 1342.5 | 64.5 | 359 | 2 | GSK3B_MOUSE |
| 28 | 1341.5 | 64.5 | 359 | 2 | GSK3B_MOUSE |
| 29 | 1305.5 | 62.7 | 501 | 1 | GSK3B_MOUSE |
| 30 | 1302 | 62.6 | 402 | 2 | GSK3B_MOUSE |
| 31 | 1296 | 62.3 | 409 | 2 | GSK3B_MOUSE |

| | | | | | |
|----|--------|------|-----|---|-------------|
| 32 | 1294 | 62.2 | 423 | 2 | GSK3B_MOUSE |
| 33 | 1289.5 | 62.0 | 398 | 2 | GSK3B_MOUSE |
| 34 | 1289.5 | 62.0 | 398 | 2 | GSK3B_MOUSE |
| 35 | 1283 | 61.7 | 410 | 1 | GSK3B_MOUSE |
| 36 | 1275.5 | 61.3 | 471 | 2 | GSK3B_MOUSE |
| 37 | 1273.5 | 61.2 | 424 | 2 | GSK3B_MOUSE |
| 38 | 1273.5 | 61.2 | 471 | 2 | GSK3B_MOUSE |
| 39 | 1273 | 61.2 | 401 | 2 | GSK3B_MOUSE |
| 40 | 1271 | 61.1 | 423 | 2 | GSK3B_MOUSE |
| 41 | 1269 | 61.0 | 412 | 2 | GSK3B_MOUSE |
| 42 | 1264 | 60.7 | 394 | 2 | GSK3B_MOUSE |
| 43 | 1263.5 | 60.7 | 424 | 2 | GSK3B_MOUSE |
| 44 | 1262.5 | 60.7 | 470 | 2 | GSK3B_MOUSE |
| 45 | 1262 | 60.6 | 355 | 2 | GSK3B_MOUSE |

ALIGNMENTS

| RESULT 1 | ID | Accession | Standard | PRT | AA |
|-------------|----|--|-------------|-----|----|
| GSK3B_HUMAN | AC | P49841 | GSK3B_MOUSE | | |
| GSK3B_HUMAN | DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| GSK3B_HUMAN | DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| GSK3B_HUMAN | DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| GSK3B_HUMAN | DT | Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta). | | | |
| GSK3B_HUMAN | GN | Name=GSK3B; | | | |
| GSK3B_HUMAN | OS | Human sapiens (Human). | | | |
| GSK3B_HUMAN | OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| GSK3B_HUMAN | OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; | | | |
| GSK3B_HUMAN | OC | Home | | | |
| GSK3B_HUMAN | OC | NCBI_TaxID=9606; | | | |
| GSK3B_HUMAN | OC | [1] | | | |
| GSK3B_HUMAN | OC | NUCLEOTIDE SEQUENCE (ISOFORM 1). | | | |
| GSK3B_HUMAN | OC | MEDLINE=95071278; PubMed=7980435; | | | |
| GSK3B_HUMAN | OC | Stambolic V., Woodgett J.R.; | | | |
| GSK3B_HUMAN | OC | "Mitogen inactivation of glycogen synthase kinase-3 beta in intact | | | |
| GSK3B_HUMAN | OC | cells via serine 9 phosphorylation."; | | | |
| GSK3B_HUMAN | OC | Biochem. J. 303:701-704(1994). | | | |
| GSK3B_HUMAN | OC | [2] | | | |
| GSK3B_HUMAN | OC | NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORMS 1 AND 2). | | | |
| GSK3B_HUMAN | OC | TISUE=Eye, and Placenta; | | | |
| GSK3B_HUMAN | OC | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | |
| GSK3B_HUMAN | OC | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| GSK3B_HUMAN | OC | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | |
| GSK3B_HUMAN | OC | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |
| GSK3B_HUMAN | OC | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| GSK3B_HUMAN | OC | Diachenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L., | | | |
| GSK3B_HUMAN | OC | Scapleton M., Soares M.B., Bonaldo M.F., Caavaud T.L., Scheetz T.E., | | | |
| GSK3B_HUMAN | OC | Brownstein M.J., Ueda T.B., Toshiyuki S., Carrini P., Prange C., | | | |
| GSK3B_HUMAN | OC | Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | | |
| GSK3B_HUMAN | OC | Boeske S.A., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| GSK3B_HUMAN | OC | Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., | | | |
| GSK3B_HUMAN | OC | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| GSK3B_HUMAN | OC | Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., | | | |
| GSK3B_HUMAN | OC | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| GSK3B_HUMAN | OC | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| GSK3B_HUMAN | OC | Rodriguez A.C., Gilmour J., Schmutz J., Myers R.M., | | | |
| GSK3B_HUMAN | OC | Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalins D.E., | | | |
| GSK3B_HUMAN | OC | Schmerer A., Schin J.E., Jones S.J.M., Matra M.A., | | | |
| GSK3B_HUMAN | OC | "Generation and initial analysis of more than 15,000 full-length human | | | |
| GSK3B_HUMAN | OC | and mouse cDNA sequences."; | | | |
| GSK3B_HUMAN | OC | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | |
| GSK3B_HUMAN | OC | [3] | | | |
| GSK3B_HUMAN | OC | NUCLEOTIDE SEQUENCE OF 185-202. | | | |
| GSK3B_HUMAN | OC | MEDLINE=99455114; PubMed=10523816; DOI=10.1038/esj.mp.4000538; | | | |
| GSK3B_HUMAN | OC | Rhoads A.R., Karkera J.D., Decker-Wadleigh S.D., | | | |
| GSK3B_HUMAN | OC | "Radiation hybrid mapping of genes in the lithium-sensitive wnt | | | |
| GSK3B_HUMAN | OC | signaling pathway."; | | | |
| GSK3B_HUMAN | OC | Mol. Psychiatry 4:437-442(1999). | | | |
| GSK3B_HUMAN | OC | [4] | | | |
| GSK3B_HUMAN | OC | NUCLEOTIDE SEQUENCE OF 1-28. | | | |

RX MEDLINE=99417672; PubMed=10486203; DOI=10.1006/geno.1999.5875;
 RA Lau K.F., Miller C.C.J., Anderson B.H., Shaw P.C.;
 RT "Molecular cloning and characterization of the human glycogen synthase
 kinase-3beta promoter."; *Genomics* 60:121-128(1999).
 RL [5]
 RN CHARACTERIZATION.
 RP MEDLINE=98409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;
 RX Delcommenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedar S.;
 RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
 synthase kinase 3 and protein kinase B/AKT by the integrin-linked
 kinase."; *Proc. Natl. Acad. Sci. U.S.A.* 95:11211-11216(1998).
 RL [6]
 RN INTERACTION WITH NIN.
 RP MEDLINE=20461863; PubMed=11004522; DOI=10.1016/S0167-4781(00)00127-5;
 RX Hong Y.-R., Chen C.-H., Chang J.-H., Wang S.-K., Sy W.-D., Chou C.-K.,
 RA Hwang S.-L.;
 RT "Cloning and characterization of a novel human ninein protein that
 interacts with the glycogen synthase kinase 3beta."; *Biochim. Biophys. Acta* 1492:513-516(2000).
 RL [7]
 RN PHOSPHORYLATION SITE THR-390.
 RP PubMed=15302935; DOI=10.1073/pnas.0404720101;
 RX Beaulieu S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
 RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
 RT "Large-scale characterization of HeLa cell nuclear phosphoproteins."; *Proc. Natl. Acad. Sci. U.S.A.* 101:12130-12135(2004).
 RL [8]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 35-386.
 RP MEDLINE=21605727; PubMed=11738041; DOI=10.1016/S0092-8674(01)00374-9;
 RX DeJani R., Fraser E., Roe S.M., Young N., Good V., Dale T.C.,
 RA Pearl L.H.;
 RT "Crystal structure of glycogen synthase kinase 3 beta: structural
 basis for phosphate-primed substrate specificity and autoinhibition."; *Cell* 105:721-732(2001).
 RL [9]
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 27-393 OF PHOSPHORYLATED
 RP GSK3B.
 RX MEDLINE=21605727; PubMed=11738041; DOI=10.1016/S0092-8674(01)00374-9;
 RA Bax B., Carter P.S., Lewis C., Guy A.R., Bridges A., Tanner R.,
 RA Petman G., Mannix C., Culbert A.A., Brown M.D.B., Smith D.G.,
 RA Reich A.D.;
 RT "The structure of phosphorylated GSK-3beta complexed with a peptide,
 FRATIDE, that inhibits beta-catenin phosphorylation."; *Structure* 9:1143-1152(2001).
 RL [10]
 RN FUNCTION: Participates in the Wnt signaling pathway. Implicated in
 the hormonal control of several regulatory proteins including
 glycogen synthase, MYB and the transcription factor JUN.
 CC Phosphorylates JUN at sites proximal to its DNA-binding domain,
 thereby reducing its affinity for DNA.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1 ENZYME REGULATION: Inhibited when phosphorylated by AKT1.
 CC -1 SUBUNIT: Monomer (by similarity). Interacts with NIN.
 CC -1 INTERACTION: G726N3:UPF3A; NBEXP=1; InAcct=EBI-373586, EBI-372587;
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49841-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49841-2; Sequence=VSP_004790;
 CC Note=No experimental confirmation available;
 CC -1 TISSUE SPECIFICITY: Expressed in testis, thymus, prostate and
 ovary and weakly expressed in lung, brain and kidney.
 CC -1 PTM: Phosphorylated by AKT1 and ILK1.
 CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
 subfamily.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not

CC removed.
 CC -----
 CC EMBL: L33801; AAA66475.1; -; mRNA.
 DR EMBL: BC000251; AAH00251.1; -; mRNA.
 DR EMBL: BC012760; AAH12760.1; -; mRNA.
 DR EMBL: AF098789; AAC69340.1; -; Genomic DNA.
 DR EMBL: AF074333; AAD48517.1; -; Genomic DNA.
 DR PIR: S53324; S53324.
 DR PDB: 1GN3; X-ray; A/B=27-393.
 DR PDB: 1H8F; X-ray; A/B=35-386.
 DR PDB: 1I09; X-ray; A/B=1-420.
 DR PDB: 1J1B; X-ray; A/B=1-420.
 DR PDB: 1J1C; X-ray; A/B=1-420.
 DR PDB: 1O9U; X-ray; A=35-384.
 DR PDB: 1PYX; X-ray; A/B=1-420.
 DR PDB: 1Q3D; X-ray; A/B=2-420.
 DR PDB: 1Q3V; X-ray; A/B=2-420.
 DR PDB: 1Q41; X-ray; A/B=2-420.
 DR PDB: 1Q4L; X-ray; A/B=2-420.
 DR PDB: 1Q5K; X-ray; A/B=7-420.
 DR PDB: 1R0S; X-ray; A/B=35-420.
 DR PDB: 1UV5; X-ray; A=35-384.
 DR InAcct: P49841; -;
 DR Ensembl: ENSG00000082701; Homo sapiens.
 DR HGNC: HGNC:4617; GSK3B.
 DR H-InvDB: HIX0003589; -;
 DR MIM: 605004; -;
 DR GO: GO:0004696; F:glycogen synthase kinase 3 activity; TAS.
 DR GO: GO:0005977; P:glycogen metabolism; TAS.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser thr pkin AS.
 DR InterPro: IPR002290; Ser thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR 3D-structure: Alternative splicing; ATP-binding; Kinase;
 KM Multisite family; Nucleotide-binding; Phosphorylation;
 KM Serine/threonine-protein kinase; transferase; Wnt signaling pathway.
 FT DOMAIN 56 340
 FT NP_BIND 62 70
 FT ACT_SITE 181 181
 FT BINDING 85 85
 FT MOD_RES 9 9
 FT MOD_RES 216 216
 FT MOD_RES 390 390
 FT VARSPPLIC 303 303
 FT MUTAGEN 9 9
 FT -----
 FT CONFLICT 28 28
 FT CONFLICT 350 350
 FT STRAND 30 30
 FT TURN 32 33
 FT STRAND 36 44
 FT STRAND 32 44
 FT STRAND 52 63
 FT STRAND 68 75
 FT STRAND 81 90
 FT TURN 91 92
 FT TURN 96 103
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 112 119
 FT STRAND 125 133
 FT STRAND 138 138
 FT STRAND 139 148
 FT TURN 149 150
 FT TURN 155 150
 FT TURN 175 176
 FT STRAND 177 178

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FT HELIX 184 186
FT STRAND 187 189
Query Match 96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.9e-13;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYTDTK 70
DB 1 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYTDTK 60
QY 71 VIGSGFQGVYQAKLCDSGELVAIKCVLODKRFKQRELOIMKLDHCNIVLRARYEYSSG 130
DB 61 VIGSGFQGVYQAKLCDSGELVAIKCVLODKRFKQRELOIMKLDHCNIVLRARYEYSSG 120
QY 131 EKKDEVYLVLDVPEVTVYVARRHSRAKOTLPVTVYKLVYMYQLFRSLAYIHSGICHR 190
DB 121 EKKDEVYLVLDVPEVTVYVARRHSRAKOTLPVTVYKLVYMYQLFRSLAYIHSGICHR 180
QY 191 DIKQNLILDPTAVLKLCDPFGSAKQVYRGEPPNYSYCSRYRAPELLFGATDYSSIDV 250
DB 181 DIKQNLILDPTAVLKLCDPFGSAKQVYRGEPPNYSYCSRYRAPELLFGATDYSSIDV 240
QY 251 MSACGVLAELLGQPIFGDSGVOLVRIKVLGPTREQIREMNPNTPEPKYKAP 310
DB 241 MSACGVLAELLGQPIFGDSGVOLVRIKVLGPTREQIREMNPNTPEPKYKAP 300
QY 311 WTKVFRPTPEPALACSRLEYYTPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPALACSRLEYYTPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTQELSSNPPLATILIPPHARI 394
DB 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 2
GSK3B MOUSE STANDARD; PRT; 420 AA.
ID GSK3B_MOUSE
AC Q9WV60;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 13-SEP-2005 (Rel. 48; Last annotation update)
DE Glycogen synthase kinase-3 beta (BC 2.7.1.37) (GSK-3 beta).
GN Name=Gsk3b;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Testis;
RA Salameh W.A., Guo T.B., Chan K.C., Mitchell A.P.;
RT "Testicular expression and hormonal control of glycogen synthase
kinase 3, a homologue of yeast RIM1.",
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Czech II, and FVB/N. TISSUE=Mammary gland;
RX MEDLINE=22386257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stempleon M., Soares W.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.H.,
RA Butlerfield Y.S.N., Kizyivski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903 (2002).
CC -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC the hormonal control of several regulatory proteins including
CC the glycogen synthase, MYB and the transcription factor JUN (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Monomer. Interacts with NIN (By similarity).
CC -1- PTM: Phosphorylation on Tyr-216 is necessary for the activity (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC subfamily.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, AF156099; AACJ9258.2; -; mRNA.
CC EMBL, BC006936; AAH06936.1; -; mRNA.
CC EMBL, BC060743; AAH060743.1; -; mRNA.
CC HSSP; P49841; 1GNG.
CC SMR; Q9WV60; 23-386.
CC Ensembl; ENSMUSG0000022812; Mus musculus.
DR MGI; MGI:1861437; Gsk3b.
DR GO; GO:0005829; C:cyclool; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0008033; F:beta-catenin binding; IPT.
DR GO; GO:0050321; F:tau-protein kinase activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IMP.
DR GO; GO:0008283; P:cell proliferation; TMS.
DR GO; GO:0045444; P:fat cell differentiation; IDA.
DR GO; GO:0009887; P:organoogenesis; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR GO; GO:0006611; P:protein-nucleus export; IDA.
DR GO; GO:0000320; P:re-entry into mitotic cell cycle; IDA.
DR GO; GO:0006950; P:response to stress; IDA.
DR GO; GO:0006950; P:response to stress; IDA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Multigene family; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase;
KW Wnt signaling pathway.
FT DOMAIN 56 340 Protein kinase.
FT NP_BIND 62 70 ATP (By similarity).
FT ACT_SITE 181 181 Proton acceptor (By similarity).
FT BINDING 85 85 ATP (By similarity).
FT MOD_RES 9 9 Phosphoserine (By PKA/AKT1) (By
FT similarity).
FT MOD_RES 216 216 Phosphotyrosine (By similarity).
SQ SEQUENCE 420 AA; 46710 MW; 200C3FD1B3844883 CRC64;

Query Match 96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.9e-13;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYTDTK 70
DB 1 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYTDTK 60

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Qy 71 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRFKRNRELOIMRLDHCNIVRLAYFFYS5G 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRFKRNRELOIMRLDHCNIVRLAYFFYS5G 120
Qy 131 EKKDEVYLNVLVDYBETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYHSFGICHR 190
Db 121 EKKDEVYLNVLVDYBETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYHSFGICHR 180
Qy 191 DIXPQNLLDPDPTAVLKLCPFGSAKQLVREPNVSYICSRYYRAPBELIFGATDYSIDV 250
Db 181 DIXPQNLLDPDPTAVLKLCPFGSAKQLVREPNVSYICSRYYRAPBELIFGATDYSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTGPTREQIRENNPNTYEFKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTGPTREQIRENNPNTYEFKFPQIKAMP 300
Qy 311 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLEACAHSPFDELADPNVKHPNGRDPALF 370
Db 301 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLEACAHSPFDELADPNVKHPNGRDPALF 360
Qy 371 NPTTQELSSNPPLATILIPPHARI 394
Db 361 NPTTQELSSNPPLATILIPPHARI 384

RESULT 3
06F127_HUMAN PRELIMINARY; PRT; 420 AA.
ID 06F127_HUMAN PRELIMINARY; PRT; 420 AA.
AC 06F127;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE GSK3B protein.
GN Name=GSK3B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiinae;
OC Homo.
NCBI_TaxID=9606;
RN NCLECTIDE SEQUENCE.
RP Halleck A., Ebert L., Moundinya M., Schick M., Bisenstein S.,
RA Neuber P., Ketrang K., Schacten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CR536510; CA38748.1; -; mRNA.
DR SMR; Q6F127; 23-386.
DR Ensembl; ENSG00000082701; Homo sapiens.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 4ACC24D00CDBB9C3 CRC64;

Query Match 96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.9e-11;
Matches 383; Conservative 0; Mismatch 1; Indels 0; Gaps 0;
Qy 11 MSGRPRTTSPAESCKPVQGSAPFSMKVSRDKDGSKVTTVATVATGCGDRPQEVSYDTK 70
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Db 1 MSGRPRTTSPAESCKPVQGSAPFSMKVSRDKDGSKVTTVATVATGCGDRPQEVSYDTK 60
Qy 71 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRFKRNRELOIMRLDHCNIVRLAYFFYS5G 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRFKRNRELOIMRLDHCNIVRLAYFFYS5G 120
Qy 131 EKKDEVYLNVLVDYBETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYHSFGICHR 190
Db 121 EKKDEVYLNVLVDYBETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYHSFGICHR 180
Qy 191 DIXPQNLLDPDPTAVLKLCPFGSAKQLVREPNVSYICSRYYRAPBELIFGATDYSIDV 250
Db 181 DIXPQNLLDPDPTAVLKLCPFGSAKQLVREPNVSYICSRYYRAPBELIFGATDYSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTGPTREQIRENNPNTYEFKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLTGPTREQIRENNPNTYEFKFPQIKAMP 300
Qy 311 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLEACAHSPFDELADPNVKHPNGRDPALF 370
Db 301 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLEACAHSPFDELADPNVKHPNGRDPALF 360
Qy 371 NPTTQELSSNPPLATILIPPHARI 394
Db 361 NPTTQELSSNPPLATILIPPHARI 384

RESULT 4
05KU03_MOUSE PRELIMINARY; PRT; 420 AA.
ID 05KU03_MOUSE PRELIMINARY; PRT; 420 AA.
AC 05KU03;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Glycogen synthase kinase 3b, last annotation update)
DE Glycogen synthase kinase 3 beta/tau protein kinase I.
GN Name=Gsk3b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NCLECTIDE SEQUENCE.
RP Sano Y., Nakano A., Hirai K., Ohta S., Yanagisawa M., Sato S.,
RA Tanori K.;
RT structures";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB066114; BAB6827.1; -; mRNA.
DR SMR; Q5KU03; 23-386.
DR Ensembl; ENSMUSG0000002812; Mus musculus.
DR MGI; MGI:1861437; Gsk3b.
DR GO; GO:0005829; C:cytosol; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0008013; F:beta-catenin binding; IPI.
DR GO; GO:00050321; F:tau-protein kinase activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IMP.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0045444; P:fat cell differentiation; IEA.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006611; P:protein-nucleus export; IEA.
DR GO; GO:0000320; P:pre-entry into mitotic cell cycle; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
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DR SMART: SM00219; TyrKc: 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 420 AA; 46710 MW; 200C3FD1388A683 CRC64;

Query Match 96.7%; Score 2013; DB 2; Length 420;
 Best Local Similarity 99.7%; Pred. No. 4.9e-131;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGQGPDRPOEVSYTDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGQGPDRPOEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCSGELVAIKVLODRKFKRELQIMRKLDHCNIVLRFFVSSG 130
 DB 61 VINGSGFVVYQAKLCSGELVAIKVLODRKFKRELQIMRKLDHCNIVLRFFVSSG 120

QY 131 EKKDEVYLVLDVYPETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKKDEVYLVLDVYPETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 180

QY 191 DIKQNLDDPDYAVLKICDPGSAQVLRGEPNVYSISRYRABELLFGATDYSSIDV 250
 DB 181 DIKQNLDDPDYAVLKICDPGSAQVLRGEPNVYSISRYRABELLFGATDYSSIDV 240

QY 251 MSAGCVLAEILLGQVIFPGDSVDQVLEIKVIGTPTRERQIREMKNPNYTEFAPQIKAMP 310
 DB 241 MSAGCVLAEILLGQVIFPGDSVDQVLEIKVIGTPTRERQIREMKNPNYTEFAPQIKAMP 300

QY 311 WTKVFRPTPEPAIALCSRLLEYTETARLTPLACAHSPFELARDPNYKHPGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTETARLTPLACAHSPFELARDPNYKHPGRDTPALF 360

QY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 5
 GSK3B_RAT STANDARD; PRT; 420 AA.
 ID GSK3B_RAT
 AC P18266;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta) (Factor A) (FA).
 DB (FA).
 GN Name=Gsk3b;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=90316097; PubMed=2164470;
 RA Woodgett J.R.;
 RT "Molecular cloning and expression of glycogen synthase kinase-3/factor A";
 RL EMBO J. 9:2431-2438(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=93307488; PubMed=7686508; DOI=10.1016/0014-5793(93)81066-9;
 RA Ishiguro K., Shiratani A., Sato S., Omori A., Arioka M., Kobayashi S., Uchida T., Imahori K.;
 RT "Glycogen synthase kinase 3 beta is identical to tau protein kinase I generating several epitopes of paired helical filaments";
 RL FEBS Lett. 325:167-172(1993).

RN [3]
 RP PHOSPHORYLATION SITE TYR-216.
 RX MEDLINE=93178457; PubMed=8382613;
 RA Hughes K., Nikolakaki S., Plyce S.E., Totty N.F., Woodgett J.R.;
 RT "Modulation of the glycogen synthase kinase-3 family by tyrosine phosphorylation";
 RL EMBO J. 12:803-808(1993).
 CC -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in the hormonal control of several regulatory proteins including glycogen synthase, MYB and the transcription factor JUN.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Interacts with NIN (By similarity). Monomer.
 CC -1- PM: Phosphorylation of Tyr-216 is necessary for the activity.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3 subfamily.
 CC -----
 CC DR EMBL; X53428; CAA37519.1; -; mRNA.
 CC DR EMBL; X73653; CAA52020.1; -; mRNA.
 CC DR PIR; S14708; TYRKB.
 CC DR HSSP; P49841; 1109.
 CC DR SMK; P18266; 23-386.
 CC DR Ensembl; ENSRN00000002833; Rattus norvegicus.
 CC DR RGP; 70982; Gsk3b.
 CC DR GO; GO:0004696; F:glycogen synthase kinase 3 activity; IDA.
 CC DR GO; GO:0005515; F:protein binding; IDA.
 CC DR GO; GO:0030010; P:establishment of cell polarity; IDA.
 CC DR GO; GO:0006917; P:induction of apoptosis; IDA.
 CC DR GO; GO:0045892; P:negative regulation of transcription, DNA-d. . .; IDA.
 CC DR InterPro; IPR000719; Prot. kinase.
 CC DR InterPro; IPR008271; Ser Thr pkin. AS.
 CC DR InterPro; IPR002290; Ser Thr kinase.
 CC DR Pfam; PF00069; Pkinase; 1.
 CC DR Prodom; PD000001; Prot. kinase; 1.
 CC DR SMART; SM00220; S_TKc; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC KW ATP-binding; Kinase; Multigene family; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
 CC KW DOMAIN 56 340 Protein kinase.
 CC FT NP_BIND 62 70 ATP (By similarity).
 CC FT ACT_SITE 181 181 Proton acceptor (By similarity).
 CC FT BINDING 85 85 ATP (By similarity).
 CC FT MOD_RES 9 9 Phosphoserine (by PKB/AKT1) (By similarity).
 CC FT MOD_RES 216 216 Phosphotyrosine.
 CC FT MUTAGEN 216 216 Y->V. Loss of phosphorylation.
 CC FT CONFLICT 240 240 M->V (in Ref. 2).
 CC SQ SEQUENCE 420 AA; 46742 MW; 2F473FCA8984398 CRC64;

Query Match 96.6%; Score 2010; DB 1; Length 420;
 Best Local Similarity 99.5%; Pred. No. 7.9e-131;
 Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGQGPDRPOEVSYTDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGQGPDRPOEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCSGELVAIKVLODRKFKRELQIMRKLDHCNIVLRFFVSSG 130
 DB 61 VINGSGFVVYQAKLCSGELVAIKVLODRKFKRELQIMRKLDHCNIVLRFFVSSG 120

QY 131 EKKDEVYLVLDVYPETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKKDEVYLVLDVYPETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 180

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Qy 191 DIKQNLDPDPVAVLKLCDPFGSAKQVLRGEPNVSYICSRYYRABELLFGATDYTSSIDV 250
Db 181 DIKQNLDPDPVAVLKLCDPFGSAKQVLRGEPNVSYICSRYYRABELLFGATDYTSSIDM 240
Qy 251 WSAGCVLAELLGQPIFPDGSQVDQVLEIIKVLGTPTRQI REMNPVYTFKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIKVLGTPTRQI REMNPVYTFKFPQIKAMP 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELBDPVRKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELBDPVRKHPNGRDTPALF 360
Qy 371 NFTQELSSNPPLATILIPPHARI 394
Db 361 NFTQELSSNPPLATILIPPHARI 384

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RESULT 6
Q5YJC2 SPECI PRELIMINARY; PRT; 420 AA.

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ID Q5YJC2 SPECI PRELIMINARY; PRT; 420 AA.
AC Q5YJC2
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Glycogen synthase kinase 3 beta.
OS Sperophilus citellus (European musk) (Citellus citellus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Sciuridae; Sciurinae; Spermophilus.
OX NCBI_TaxId=9997;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stefeler J.T., Strijkstra A.M.;
RT "Molecular cloning of Spermophilus citellus glycogen synthase kinase 3
beta."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY392021; AAS59774.1; -, mRNA.
DR SMR: Q5YJC2; 23-386.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 5F5243CA7D9E3549 CRC64;

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Query Match 96.4%; Score 2006; DB 2; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.5e-130;
Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 11 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKGSKVTTVATRGQGDPRQEVSYTDK 70
Db 1 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKGSKVTTVATRGQGDPRQEVSYTDK 60
Qy 71 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 130
Db 61 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 120
Qy 131 EKQDEVLTNLVDVPEVTVVVAHYSRAKQTLPIVYKLYMYQLFRSLAYHSFGICHR 190

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Db 121 EKQDEVLTNLVDVPEVTVVVAHYSRAKQTLPIVYKLYMYQLFRSLAYHSFGICHR 180
Qy 191 DIKQNLDPDPVAVLKLCDPFGSAKQVLRGEPNVSYICSRYYRABELLFGATDYTSSIDV 250
Db 181 DIKQNLDPDPVAVLKLCDPFGSAKQVLRGEPNVSYICSRYYRABELLFGATDYTSSIDM 240
Qy 251 WSAGCVLAELLGQPIFPDGSQVDQVLEIIKVLGTPTRQI REMNPVYTFKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFPDGSQVDQVLEIIKVLGTPTRQI REMNPVYTFKFPQIKAMP 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELBDPVRKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELBDPVRKHPNGRDTPALF 360
Qy 371 NFTQELSSNPPLATILIPPHARI 394
Db 361 NFTQELSSNPPLATILIPPHARI 384

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RESULT 7
Q91BD2 BRABE PRELIMINARY; PRT; 421 AA.

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ID Q91BD2 BRABE PRELIMINARY; PRT; 421 AA.
AC Q91BD2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Glycogen synthase kinase 3 beta.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RX Shimizu T., Yamamaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bcozox/K/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish."
RL Mech. Dev. 91:293-303(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AB032265; BAA92442.1; -, mRNA.
DR HSSP: P49841; 1109.
DR SMR: Q91BD2; 23-386.
DR Ensemble: ENSDARG0000017803; Danio rerio.
DR ZFIN: ZDB-GENE-990714-4; gsk3b.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46856 MW; 2B251B4C66C000EB CRC64;

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Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 2.7e-127;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy 11 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKGSKVTTVATRGQGDPRQEVSYTDK 70
Db 1 MSGRPRTTSFAESCKPVOQPSAFSGMKVSRDKGSKVTTVATRGQGDPRQEVSYTDK 60
Qy 71 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 130

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Db 61 VIGNSFGVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCIVLRLRYFFSSG 120
Qy 131 EKKDEVYLVLDVPEYTVVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
Db 121 DKDEVYLVLDVPEYTVVVARHYSRAKOTLPVYVYKLYMYOLFSLAYIHSFGICHR 180
Qy 191 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 250
Db 181 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 240
Qy 251 MSACGVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRREQIREMNPNTTEKFPQIKAH 310
Db 241 MSACGVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRREQIREMNPNTTEKFPQIKAH 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELADPNVKGHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELADPNVKGHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHAR 393
Db 361 NFTTOELSSNPPLATILIPPHAR 383
RESULT 8
Q9YH60_BRARE PRELIMINARY; PRT; 421 AA.
AC Q9YH60;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glycogen synthase kinase 3.
GN Name=gsk3b; Synonyms=GSK3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=20173069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
RT "Differential expression of glycogen synthase kinase 3 genes during
RT zebrafish embryogenesis";
RL Mech. Dev. 91:387-391(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ223502; CA111420.1; -, mRNA.
DR HSSP; P49841; 1109.
DR SMK; Q9YH60; 23-386.
DR Ensembl; ENSDARG0000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; KINASE; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46872 MW; 2B51B4C7B6C00EB CRC64;
Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 2.7e-127;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Qy 11 MSGRPTTSFASCKPVPQPSAFSGSMKYSRDKDGSKTTVTVAATPGCGDRPOEVSYTDTK 70

Db 1 MSGRPTTSFASCKPVPQPSAFSGSMKYSRDKDGSKTTVTVAATPGCGDRPOEVSYTDTK 60
Qy 71 VIGNSFGVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCIVLRLRYFFSSG 130
Db 61 VIGNSFGVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCIVLRLRYFFSSG 120
Qy 131 EKKDEVYLVLDVPEYTVVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
Db 121 DKDEVYLVLDVPEYTVVVARHYSRAKOTLPVYVYKLYMYOLFSLAYIHSFGICHR 180
Qy 191 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 250
Db 181 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 240
Qy 251 MSACGVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRREQIREMNPNTTEKFPQIKAH 310
Db 241 MSACGVLAELLGQPIFGDGSVDQVLEIIVKLGTPTRREQIREMNPNTTEKFPQIKAH 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELADPNVKGHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELADPNVKGHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHAR 393
Db 361 NFTTOELSSNPPLATILIPPHAR 383
RESULT 9
Q91757_XENLA PRELIMINARY; PRT; 420 AA.
AC Q91757;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Intracellular kinase.
GN Name=xgsk-3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=95237008; PubMed=7720580;
RA Pierce S.B., Knehlman D.;
RT "Regulation of Spemann organizer formation by the intracellular kinase
RT Xgsk-3";
RL Development 121:755-765(1995).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L38492; AAC42224.1; -, mRNA.
DR PIR; I51425; I51425.
DR HSSP; P49841; 1109.
DR SMK; Q91757; 23-386.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46903 MW; C02280B8A35785D CRC64;
Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 2.3e-125;

Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKGSKTTTVAATPGQDPDPQEVSYDTK 70
 DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKGSKTTTVAATPGQDPDPQEVSYDTK 60
 QY 71 VINGSGFGVYVQAKLDCSGELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 130
 DB 61 VINGSGFGVYVQAKLDCSGELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 120
 QY 131 EKKDEVYLVLDVPEPTVYRVARHYSRAKQTLPIVYKLYMQLFRSLAYHSFGICHR 190
 DB 121 EKKDEVYLVLDVPEPTVYRVARHYSRAKQALPIVYKLYMQLFRSLAYHSFGICHR 180
 QY 191 DIKQNLDDPDTAVLKDCFGSAKQVLRGEPNVSYCSRYRAPBELFGATDVTSSIDV 250
 DB 181 DIKQNLDDPDTAVLKDCFGSAKQVLRGEPNVSYCSRYRAPBELFGATDVTSSIDV 240
 QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPYTEFKEFPQIKAH 310
 DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPYTEFKEFPQIKAH 300
 QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
 QY 371 NFTTQELSSNPPLATIIIPPHAR 393
 DB 361 NFTTQELSSNPPLATIIIPPHAR 383

RESULT 10
 091627_XENLA PRELIMINARY; PRT; 420 AA.

ID 091627;
 AC 091627;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Glycogen synthase kinase 3 beta.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95396823; PubMed=7667318;
 RA Dominguez I., Itoh K., Sokol S.Y.;
 RT "Role of glycogen synthase kinase 3 beta as a negative regulator of
 RT dorsoventral axis formation in Xenopus embryos.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:8498-8502(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: U31862; AA84444.1; -; mRNA.
 DR PIR: I51692; I51692.
 DR HSSP: P49841; 1109.
 DR SMR: 091627; 23-386.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004678; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser_thr_kin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: P00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SMO0220; S_TK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
 KM Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 420 AA; 46900 MW; 4FECCEA381835BFC7 CRC64;

Query Match 92.4%; Score 1923; DB 2; Length 420;
 Best Local Similarity 95.0%; Pred. No. 8.2e-125;
 Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKGSKTTTVAATPGQDPDPQEVSYDTK 70
 DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKGSKTTTVAATPGQDPDPQEVSYDTK 60
 QY 71 VINGSGFGVYVQAKLDCSGELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 130
 DB 61 VINGSGFGVYVQAKLDCSGELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 120
 QY 131 EKKDEVYLVLDVPEPTVYRVARHYSRAKQTLPIVYKLYMQLFRSLAYHSFGICHR 190
 DB 121 EKKDEVYLVLDVPEPTVYRVARHYSRAKQALPIVYKLYMQLFRSLAYHSFGICHR 180
 QY 191 DIKQNLDDPDTAVLKDCFGSAKQVLRGEPNVSYCSRYRAPBELFGATDVTSSIDV 250
 DB 181 DIKQNLDDPDTAVLKDCFGSAKQVLRGEPNVSYCSRYRAPBELFGATDVTSSIDV 240
 QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPYTEFKEFPQIKAH 310
 DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPYTEFKEFPQIKAH 300
 QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
 QY 371 NFTTQELSSNPPLATIIIPPHAR 393
 DB 361 NFTTQELSSNPPLATIIIPPHAR 383

RESULT 11
 04SOHO_TETNG PRELIMINARY; PRT; 496 AA.

ID 04SOHO;
 AC 04SOHO;
 DT 13-SEP-2005 (TREMblrel. 31, Created)
 DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
 DE Chromosome 2 SCAF14781, whole genome shotgun sequence.
 GN ORFNames=GSTENG0026022001;
 OS Tetradodon nigroviridis (Green puffer).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acantomorpha; Acantopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Tetraodontidae; Tetraodon.
 NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Cobaz C., Benoit A.,
 RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
 RA Dasiyla C., Salenoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellil V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cartolico L., Poulin J., De Bernardis V.,
 RA Craud C., Duprat S., Broctier P., Couranceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellie M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Landier V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope: Whitehead Institute Centre for Genome Research;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell

CC cycle. It is required in higher cells for entry into S-phase and
 CC mitosis. Component of the kinase complex that phosphorylates the
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of
 CC MPP (by similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 CC mature oocytes (by similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: CA601014781; CAG05862.1; -1 Genomic_DNA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 2.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 DR Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 496 AA; 55961 MW; 4C86362BD3301390 CRC64;

Query Match 86.2%; Score 1793.5; DB 2; Length 496;
 Best Local Similarity 73.8%; Pred. No. 9e-116; Indels 115; Gaps 3;
 Matches 354; Conservative 8; Mismatches 3;

QY 11 MSGRRRTTSFAESCKPVOQPSAFSGSMKYSR-----DKDGSKYTTVAATPGCGPPRP 61
 DB 1 MSGRRRTTSFAESCKPVPQPSAFSGSMKYSQTLNGPWRGDDGDSKYTTVAATPGCGPPRP 60
 QY 62 QEVSTDTKVIKNGSFGVYVQAKLCDSEGLVAIKKVLQDKPKFKNELQIMKLDHCNIVR 121
 DB 61 QEVSTDTKVIKNGSFGVYVQAKLCDSEGLVAIKKVLQDKPKFKNELQIMKLDHCNIVR 120
 QY 122 LRFYFSSGSK----- 132
 DB 121 LRFYFSSGSKPDRRANRPSVSNMVTGELSLWLCKPCSQLTRAVVAQAGSQEPIR 180
 QY 133 -----KDEVIYLVLDYV 145
 DB 181 PSGNPCKMLCKGRKSLFLRESANKAVDIPQVPRSRGHSYRSGSKDEVIYLVLDYV 240
 QY 146 PETVYVARYHSRAKQTLPIVYKLMYQLQFSLAYIHSFGICHRDIPQNLLDPTNAV 205
 DB 241 PETVYVARYHSRAKQTLPIVYKLMYQLQFSLAYIHSFGICHRDIPQNLLDPTNAV 300
 QY 206 LKLCDFGSAKQLVGEPVNSYICRYTPAPELIFGATDTYSSIDVWSAGCVLAELLQGP 265
 DB 301 LKLCDFGSAKQLVGEPVNSYICRYTPAPELIFGATDTYSSIDVWSAGCVLAELLQGP 360
 QY 266 IFPGDSGVQDQVLEIK-----VLGTPRQDIREMNPVYEFKFPQIKAHPTMYVF 315
 DB 361 IFPGDSGVQDQVLEIKRQNAAPRSQVIGTPRQDIREMNPVYEFKFPQIKAHPTMYVF 420
 QY 316 RPRTPPEAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDTPALFNFTTQ 375
 DB 421 RPRTPPEAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDTPALFNFTTQ 480

RESULT 12
 Q9YH61 BRARE PRELIMINARY; PRT; 440 AA.
 AC Q9YH61
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Glycogen synthase kinase 3 alpha.
 GN Name=gsk3a; Synonym=gSK3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
 RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
 RT "Differential expression of glycogen synthase kinase 3 genes during
 RT zebrafish embryogenesis.";
 RL Mech. Dev. 91:387-391(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Muliahy S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Straubeberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AJ223501; CA111419.1; -; mRNA.
 DR EMBL: BC065952; AAH65952.1; -; mRNA.
 DR EMBL: BC066332; AAH66332.1; -; mRNA.
 DR HSSP: P49841; 1Q3W.
 DR SMK: Q9YH61; 52-412.
 DR Ensembl: ENSDARG0000015681; Danio rerio.
 DR ZFIN: ZDB-GENE-990714-3; gsk3a.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 440 AA; 48065 MW; 66A88BD070AC2A093 CRC64;

Query Match 81.9%; Score 1704.5; DB 2; Length 440;
 Best Local Similarity 79.1%; Pred. No. 1.1e-109;
 Matches 326; Conservative 26; Mismatches 25; Indels 35; Gaps 3;
 12 SGRPRRTTSFAESCKPVOQPSAFSGSMKYSR-----SFGSMKYSRD 41

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Db 4 SGRPRITSSFAE---PGVPFGAAAAAGSAVAGSSSGKTGGAQAAGSSSGFGLNKLKGR- 59
Qy 42 KDGSKVTTVVATPGCGPDRPOEVSYTDTKYINGSGFGVYVYQAKLCDSEGLVATIKVLODK 101
Db 60 -DSGKVTTVVATPGCGPDRPOEVSYTDIKVINGSGFGVYVYQARLIDSEMAVATIKVLODK 118
Qy 102 RFKRELQIMRKLDHCNIVLRARFFYSGGKDEVLNLVLDVYPETVYVAAHYSPRAKQ 161
Db 119 RFKRELQIMRKLDHCNIVLRARFFYSGGKDEVLNLVLDVYPETVYVAAHYSPRAKQ 178
Qy 162 TLPVIYKLYMYQLFRSLAYIHSFGICHRDIKQNLILDPDTAVLKLCDFGSAKQVLRGE 221
Db 179 TIFPIYKVMYQLFRSLAYIHSQGVCHRDIKPNLNLVDPTAVLKLCDFGSAKQVLRGE 238
Qy 222 PNVSYICSRYYRABELIFGATDYTSNIDWSAGCVLAELLGQPIFPDGSQVQLVEIIT 281
Db 239 PNVSYICSRYYRABELIFGATDYTSNIDWSAGCVLAELLGQPIFPDGSQVQLVEIIT 298
Qy 282 VLGPTREQIREKMPNTEFEKFPQIKAPMTKVFPRPTPEAALCSRLLEYTPARLTP 341
Db 299 VLGPTREQIREKMPNTEFEKFPQIKAPMTKVFPRPTPEAALCSRLLEYTPARLTP 358
Qy 342 LEACAHSFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 359 LEACAHAFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 410

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RESULT 13
Q9IBD3 BRARE
ID Q9IBD3 BRARE PRELIMINARY; PRT; 435 AA.
AC Q9IBD3
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Glycogen synthase kinase 3 alpha.
GN Name=gsk3a;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN NM_017105.1;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RA Shimizu T., Yamamaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.,
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish."
RT Mech. Dev. 91:293-303(2000).
RL Mech. Dev. 91:293-303(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB032264; BAA92441.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9IBD3; 52-412.
DR Ensembl; ENSDARG00000029723; Danio rerio.
DR ZFIN; ZDB-GENE-990714-3; gsk3a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 435 AA; 47791 MW; ED77993A03D8C706 CRC64;

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Query Match 80.2%; Score 1669.5; DB 2; Length 435;
Best Local Similarity 78.2%; Pred. No. 2,9e-107;
Matches 322; Conservative 26; Mismatches 29; Indels 35; Gaps 3;
Qy 12 SGRPRITSSFAE---PGVPFGAAAAAGSAVAGSSSGKTGGAQAAGSSSGFGLNKLKGR- 59
Db 4 SGRPRITSSFAE---PGVPFGAAAAAGSAVAGSSSGKTGGAQAAGSSSGFGLNKLKGR- 59
Qy 42 KDGSKVTTVVATPGCGPDRPOEVSYTDTKYINGSGFGVYVYQAKLCDSEGLVATIKVLODK 101
Db 60 -DSGKVTTVVATPGCGPDRPOEVSYTDIKVINGSGFGVYVYQARLIDSEMAVATIKVLODK 118
Qy 102 RFKRELQIMRKLDHCNIVLRARFFYSGGKDEVLNLVLDVYPETVYVAAHYSPRAKQ 161
Db 119 RFKRELQIMRKLDHCNIVLRARFFYSGGKDEVLNLVLDVYPETVYVAAHYSPRAKQ 178
Qy 162 TLPVIYKLYMYQLFRSLAYIHSFGICHRDIKQNLILDPDTAVLKLCDFGSAKQVLRGE 221
Db 179 TIFPIYKVMYQLFRSLAYIHSQGVCHRDIKPNLNLVDPTAVLKLCDFGSAKQVLRGE 238
Qy 222 PNVSYICSRYYRABELIFGATDYTSNIDWSAGCVLAELLGQPIFPDGSQVQLVEIIT 281
Db 239 PNVSYICSRYYRABELIFGATDYTSNIDWSAGCVLAELLGQPIFPDGSQVQLVEIIT 298
Qy 282 VLGPTREQIREKMPNTEFEKFPQIKAPMTKVFPRPTPEAALCSRLLEYTPARLTP 341
Db 299 VLGPTREQIREKMPNTEFEKFPQIKAPMTKVFPRPTPEAALCSRLLEYTPARLTP 358
Qy 342 LEACAHSFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 359 LEACAHAFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 410

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RESULT 14
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AC Q9NL43
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Glycogen synthase kinase alpha/beta.
GN Name=CiGSK; Synonyms=Ci-GSK alpha/beta;
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cloniidae; Clona.
OC NCBI_TaxID=7719;
RN NM_017105.1;
RP NUCLEOTIDE SEQUENCE.
RA Imai K., Takada N., Satoh Y.,
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB031544; BAA92186.1; -; mRNA.
DR EMBL; AB211133; BAE06824.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9NL43; 9-368.
DR Ensembl; ENSCING0000001821; Clona intestinalis.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 407 AA; 4556 MW; E71594A9B6B59F10 CRC64;

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Query Match 80.1%; Score 1666.5; DB 2; Length 407;
 Best Local Similarity 83.0%; Pred. No. 4.4e-107;
 Matches 318; Conservative 24; Mismatches 26; Indels 15; Gaps 2;

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 DB 1 MKGAPKTT-----LGNMKGSRDKE-SKITTVVATHGHPDRPQEVATDRK 45
 QY 71 VIGNSFGVYVQAKLCDSEGLVAIKKVLQDKPKFKNRELQIMRDLHCNIVRLRYFFYSGG 130
 DB 46 VIGNSFGVYVQARIESNEMVAIKKVLQDKPKFKNRELQIMRDLHCNIVRLRYFFYSGG 105
 QY 131 EKKDEYVNLVLDYVPEYTVRVARHYSKAKQTLPIVYVLYWYQLFRSLAYIHSFGICHR 190
 DB 106 DKDEYVNLVLDYVPEYTVRVARHYSKAKQTLPIVYVLYWYQLFRSLAYIHSFGICHR 165
 QY 191 DIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYTSSIDV 250
 DB 166 DIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYTSSIDV 225
 QY 251 WSAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKQIKAP 310
 DB 226 WSAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKQIKAP 285
 QY 311 WTKVRPTPPRAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKGHPGRDTPALF 370
 DB 286 WSKVRPTPPRAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKGHPGRDTPALF 345
 QY 371 NETTOELSSNPPLATILIPPHAR 393
 DB 346 NPTDKELSIKSPILNILLIPPHAR 368

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 AC Q6UG5-
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Glycogen synthase kinase-3.
 GN Name=GSK-3;
 OS Lytechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed15151983; DOI=10.1242/dev.01152;
 RA Weltzel H.E., Illies M.R., Byrum C.A., Xu R., Wikramanayake A.H.,
 RA Ettensohn C.A.;
 RT "Differential stability of {beta}-catenin along the animal-vegetal
 axis of the sea urchin embryo mediated by dishevelled.";
 RL Development 131.2947-2956(2004).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AY624076; AAT42372.1; -; mRNA.
 DR HSSP; P24941; IAO1.
 DR SMR; Q6UG5; 23-381.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_kin AS.
 DR InterPro; IPR002390; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 414 AA; 46202 MW; 276988692DF90815 CRC64;

Query Match 78.4%; Score 1632; DB 2; Length 414;
 Best Local Similarity 80.5%; Pred. No. 1.1e-104;
 Matches 306; Conservative 35; Mismatches 37; Indels 2; Gaps 1;

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 QY 72 IGNISFGVYVQAKLCDSEGLVAIKKVLQDKPKFKNRELQIMRDLHCNIVRLRYFFYSGE 131
 DB 62 IGNISFGVYVQARIVMDTNDLVAIKKVLQDKPKFKNRELQIMRDLHCNIVRLRYFFYSGE 121
 QY 132 KKDEYVNLVLDYVPEYTVRVARHYSKAKQTLPIVYVLYWYQLFRSLAYIHSFGICHRD 191
 DB 122 KKDEYVNLVLDYVPEYTVRVARHYSKAKQTLPIVYVLYWYQLFRSLAYIHSFGICHRD 181
 QY 192 IKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYTSSIDV 251
 DB 182 IKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYTCDIDV 241
 QY 252 SAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKQIKAPW 311
 DB 242 SAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKQIKAPW 301
 QY 312 TKVFRPTPPRAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKGHPGRDTPALF 371
 DB 302 SKVFRTRTPADAIQLCSRLLEYTPKSRIPLEACHQPFSELRDPIKLPHGRDLPLFN 361
 QY 372 FTTTOELSSNPPLATILIPPH 391
 DB 362 FTAGELASKPSLRTALIPPH 381

Search completed: May 16, 2006, 15:09:33
 Job time : 232 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2006, 15:09:51 ; Search time 45 Seconds
(without alignments)
723.872 Million cell updates/sec

Title: US-10-689-461-2

Sequence: 1 MEVYPMEGGSGSGRPRTTSF.....QELSSNPPLATILPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
 - 2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfilest.ppp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2081 | 100.0 | 394 | 2 | US-09-916-109-2 |
| 2 | 2081 | 100.0 | 394 | 2 | US-10-211-412B-2 |
| 3 | 2024 | 97.3 | 420 | 2 | US-09-336-038-1 |
| 4 | 2024 | 97.3 | 420 | 2 | US-09-916-109-1 |
| 5 | 2024 | 97.3 | 420 | 2 | US-10-211-412B-1 |
| 6 | 2024 | 97.3 | 420 | 2 | US-09-538-092-1163 |
| 7 | 2010 | 96.6 | 420 | 1 | US-08-602-264A-14 |
| 8 | 1883.5 | 90.5 | 361 | 2 | US-09-916-109-3 |
| 9 | 1883.5 | 90.5 | 361 | 2 | US-10-211-412B-3 |
| 10 | 1609 | 77.3 | 447 | 2 | US-09-916-109-5 |
| 11 | 1609 | 77.3 | 447 | 2 | US-10-211-412B-5 |
| 12 | 1609 | 77.3 | 483 | 2 | US-09-916-109-4 |
| 13 | 1609 | 77.3 | 483 | 2 | US-10-211-412B-4 |
| 14 | 1609 | 77.3 | 483 | 2 | US-09-538-092-1162 |
| 15 | 1588 | 76.3 | 351 | 2 | US-09-916-109-7 |
| 16 | 1588 | 76.3 | 351 | 2 | US-10-211-412B-7 |
| 17 | 1588 | 76.3 | 387 | 2 | US-09-916-109-6 |
| 18 | 1588 | 76.3 | 387 | 2 | US-10-211-412B-6 |
| 19 | 1256 | 60.4 | 412 | 2 | US-09-347-801-21 |
| 20 | 1256 | 60.4 | 412 | 2 | US-09-854-731-21 |
| 21 | 1242 | 59.7 | 410 | 2 | US-09-347-801-10 |
| 22 | 1242 | 59.7 | 410 | 2 | US-09-854-731-10 |
| 23 | 1240 | 59.6 | 402 | 2 | US-09-347-801-16 |
| 24 | 1240 | 59.6 | 402 | 2 | US-09-854-731-16 |
| 25 | 1232 | 59.2 | 405 | 2 | US-09-347-801-20 |
| 26 | 1232 | 59.2 | 405 | 2 | US-09-854-731-20 |
| 27 | 1232 | 59.2 | 407 | 2 | US-09-347-801-23 |

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| 28 | 1232 | 59.2 | 407 | 2 | US-09-854-731-23 | Sequence 23, Appl |
| 29 | 1226 | 58.9 | 411 | 2 | US-09-347-801-22 | Sequence 22, Appl |
| 30 | 1226 | 58.9 | 411 | 2 | US-09-854-731-22 | Sequence 22, Appl |
| 31 | 1165.5 | 56.0 | 399 | 2 | US-09-347-801-14 | Sequence 14, Appl |
| 32 | 1165.5 | 56.0 | 399 | 2 | US-09-854-731-14 | Sequence 14, Appl |
| 33 | 1001.5 | 48.1 | 395 | 2 | US-09-248-796A-18499 | Sequence 18499, A |
| 34 | 940 | 45.2 | 370 | 2 | US-09-538-092-623 | Sequence 623, App |
| 35 | 674 | 32.4 | 411 | 2 | US-09-248-796A-18500 | Sequence 18500, A |
| 36 | 521.5 | 25.1 | 146 | 2 | US-09-270-767-43078 | Sequence 43078, A |
| 37 | 483.5 | 23.2 | 649 | 2 | US-09-949-016-10147 | Sequence 10147, A |
| 38 | 483.5 | 23.0 | 334 | 2 | US-09-949-016-10777 | Sequence 10777, A |
| 39 | 476.5 | 22.9 | 379 | 2 | US-09-411-628-14 | Sequence 14, Appl |
| 40 | 476.5 | 22.9 | 379 | 2 | US-10-174-794-14 | Sequence 14, Appl |
| 41 | 476.5 | 22.9 | 379 | 2 | US-09-538-092-1021 | Sequence 1021, Ap |
| 42 | 472.5 | 22.7 | 379 | 2 | US-08-622-277A-8 | Sequence 8, Appl |
| 43 | 472.5 | 22.7 | 379 | 2 | US-09-025-560-25 | Sequence 25, Appl |
| 44 | 472.5 | 22.7 | 379 | 2 | US-09-642-749-25 | Sequence 25, Appl |
| 45 | 472.5 | 22.7 | 631 | 2 | US-09-417-197-39 | Sequence 39, Appl |

ALIGNMENTS

| | | | | | | | | | |
|--|-----|---|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| US-09-916-109-2 | | | | | | | | | |
| Sequence 2, Application US/09916109 | | | | | | | | | |
| Patent No. 6465231 | | | | | | | | | |
| GENERAL INFORMATION: | | | | | | | | | |
| APPLICANT: Harrison, Stephen D. | | | | | | | | | |
| APPLICANT: Hall, John A. | | | | | | | | | |
| APPLICANT: Calderon-cacia, Maria | | | | | | | | | |
| APPLICANT: Zhong, Ziyang | | | | | | | | | |
| APPLICANT: Fong, Eric Y. | | | | | | | | | |
| APPLICANT: Colt, Doris G. | | | | | | | | | |
| APPLICANT: Nguyen, Steve H. | | | | | | | | | |
| APPLICANT: Medina-seib, Angelica | | | | | | | | | |
| TITLE OF INVENTION: GSK3 POLYPEPTIDES | | | | | | | | | |
| FILE REFERENCE: PP-15876.002/200130.524 | | | | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/916.109 | | | | | | | | | |
| CURRENT FILING DATE: 2001-07-25 | | | | | | | | | |
| NUMBER OF SEQ ID NOS: 11 | | | | | | | | | |
| SOFTWARE: FastSeq for Windows Version 4.0 | | | | | | | | | |
| SEQ ID NO 2 | | | | | | | | | |
| LENGTH: 394 | | | | | | | | | |
| TYPE: PRT | | | | | | | | | |
| ORGANISM: Homo sapiens | | | | | | | | | |
| US-09-916-109-2 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Score 2081; DB 2; Length 394; | | | | | | | | | |
| Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
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| DB | 1 | MEVYPMEGGSGSGRPRTTSFASCKPVQQAFAFGSMKVRDQSGSKYTVVATGQGPDR | 60 | | | | | | |
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| DB | 61 | POEVSYDTKTVIGNGSGFVVYQAKLCDGSELVAIKVLDKRFNNRELQINRKLDCNIV | 120 | | | | | | |
| QY | 121 | RLRFFPSSGSKQDEVTINLVDPVETVYVVAHHYSAAKQTLVYIYKLYMYQLFRSLA | 180 | | | | | | |
| DB | 121 | RLRFFPSSGSKQDEVTINLVDPVETVYVVAHHYSAAKQTLVYIYKLYMYQLFRSLA | 180 | | | | | | |
| QY | 181 | YIHSFGICHRDIKQNLIDPDTAVLKLCDGSAKQLVGSPNYSYCSRYRABELIFG | 240 | | | | | | |
| DB | 181 | YIHSFGICHRDIKQNLIDPDTAVLKLCDGSAKQLVGSPNYSYCSRYRABELIFG | 240 | | | | | | |
| QY | 241 | ATDYSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVIGTPTREQIRENNPNYTE | 300 | | | | | | |
| DB | 241 | ATDYSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVIGTPTREQIRENNPNYTE | 300 | | | | | | |
| QY | 301 | KFPQIRAHPTKVFRRPTPEALALCSRLLETPTARLTPLBACAHSPFDELDPNVKH | 360 | | | | | | |

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RESULT 2

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US-10-211-412B-2
; Sequence 2, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211.412B
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916.109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-2
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Query Match 100.0%; Score 2081; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.8e-221;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 301 FKFPQIAHPTKVFRRPTPEALALCSRLLEYTPARLTPLBACAHSPFDELDPNVKH 360
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RESULT 3
US-09-336-038-1
; Sequence 1, Application US/09336038
; Patent No. 6417185
; GENERAL INFORMATION:
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; APPLICANT: Goff, Dane
; APPLICANT: Harrison, Steven
; APPLICANT: Nuse, John
; APPLICANT: Ring, David B.
; APPLICANT: Zhou, Xiaohu A.
; TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
; FILE REFERENCE: 1443.003
; CURRENT APPLICATION NUMBER: US/09/336.038
; PRIOR FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/089.978
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-038-1
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Best Local Similarity 100.0%; Pred. No. 6.3e-215;
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Db 181 DIKQNLILDDPTAVLKCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELILGQPIFGDSGVQDLVEIIVLGPTRREGIIRNNPNYTEFKFPQIAHP 310
Db 241 WSAGCVLAELILGQPIFGDSGVQDLVEIIVLGPTRREGIIRNNPNYTEFKFPQIAHP 300
Qy 311 WTKVFRPTPEALALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEALALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384
```

RESULT 4

```
US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916.109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
```



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: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-916-109-1

Query Match      97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.3e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 70
DB 1 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 130
DB 61 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 120
QY 131 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREFKMPNTEFEKFOIKAH 310
DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREFKMPNTEFEKFOIKAH 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLPLEACNSFFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLPLEACNSFFDELDPNVKHPNGRDTPALF 360
QY 371 NPTQELSSNPPLATILIPPHARI 394
DB 361 NPTQELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412B-1
: Sequence 1, Application US/10211412B
: Patent No. 6716624
: GENERAL INFORMATION:
: APPLICANT: Harrison, Stephen D.
: APPLICANT: Hall, John A.
: APPLICANT: Calderon-Cacela, Maria
: APPLICANT: Zhong, Ziyang
: APPLICANT: Fang, Eric Y.
: APPLICANT: Coit, Doris G.
: APPLICANT: Nguyen, Steve H.
: APPLICANT: Medina-Selby, Angelica
: TITLE OF INVENTION: GSK3 POLYPEPTIDES
: FILE REFERENCE: 59516-162/P-15876.002/200130.524
: CURRENT APPLICATION NUMBER: US/10/211,412B
: PRIOR FILING DATE: 2002-07-31
: PRIOR APPLICATION NUMBER: US09/916,109
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 420
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-211-412B-1

Query Match      97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.3e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 70
DB 1 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 130
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DB 61 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 120
QY 131 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREFKMPNTEFEKFOIKAH 310
DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREFKMPNTEFEKFOIKAH 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLPLEACNSFFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLPLEACNSFFDELDPNVKHPNGRDTPALF 360
QY 371 NPTQELSSNPPLATILIPPHARI 394
DB 361 NPTQELSSNPPLATILIPPHARI 384

RESULT 6
US-09-538-092-1163
: Sequence 1163, Application US/09538092
: Patent No. 6753314
: GENERAL INFORMATION:
: APPLICANT: Gluc, Loic
: APPLICANT: Mansfield, Traci A.
: TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
: FILE REFERENCE: 15966-542
: CURRENT APPLICATION NUMBER: US/09/538,092
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: 60/127,352
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: 60/178,965
: NUMBER OF SEQ ID NOS: 1387
: SOFTWARE: CuratSeqFormatter Version 0.9
: SEQ ID NO 1163
: LENGTH: 420
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: Polypeptide Accession Number P49841
US-09-538-092-1163

Query Match      97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.3e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 70
DB 1 MSGRRRTTSFAESCKPVOQPSAFSGMKVSRDKDGSKTTTVAATPGCGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 130
DB 61 VINGSGFVVYQAKLCSGSELVAIKKVLQDKRFKRELIQIMKLDHCNIIVLRKYFFYSYG 120
QY 131 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYINLVLDYVPEVTVVVAHYSRAKQTLPIYIYKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQONLLDPDTAVLKLCDFGSAKQVRGBPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREFKMPNTEFEKFOIKAH 310
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Db 241 WSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQIIRKNNPNYTEFKFPQIKAMP 300
Qy 311 WTKVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGRDTALP 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGRDTALP 360
Qy 371 NPTTOELSSNPPLATILIPPHARI 394
Db 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 7
US-08-602-264A-14
Sequence 14, Application US/08602264A
Patent No. 5837853
GENERAL INFORMATION:
APPLICANT: AKIHKO TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE
TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: human being
US-08-602-264A-14

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 2,2e-213;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQOPSAFGSMKVSBDKSGKVTTVVATPGQGPDRQOEVSYTDK 70
Db 1 MSGRPRTTSPAESCKPVQOPSAFGSMKVSBDKSGKVTTVVATPGQGPDRQOEVSYTDK 60
Qy 71 VINGSGGVVYQAKLCSGSELVAIKVLDQRFPKRELQIRKLDHCNIVLRYFFSSG 130
Db 61 LINGSGGVVYQAKLCSGSELVAIKVLDQRFPKRELQIRKLDHCNIVLRYFFSSG 120
Qy 131 EKDEVLINLVLDVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFGICHR 190
Db 131 EKDEVLINLVLDVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFGICHR 190

Db 121 EKDEVLINLVLDVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFGICHR 180
Qy 191 DIKRONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYICSHYYAPABELIFGATDVTSSIDV 250
Db 181 DIKRONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYICSHYYAPABELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQIIRKNNPNYTEFKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQIIRKNNPNYTEFKFPQIKAMP 300
Qy 311 WTKVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGRDTALP 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGRDTALP 360
Qy 371 NPTTOELSSNPPLATILIPPHARI 394
Db 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 8
US-09-916-109-3
Sequence 3, Application US/09916109
Patent No. 6465231
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876, 002/200130,524
CURRENT APPLICATION NUMBER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.8e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 MEYVPMEGGMSGRPTTSPAESCKPVQOPSAFGSMKVSBDKSGKVTTVVATPGQGPDR 60
Db 1 MEYVPMEGG-----GSKVTTVVATPGQGPDR 27
Qy 61 POEVSYTDIVYINGSGGVVYQAKLCSGSELVAIKVLDQRFPKRELQIRKLDHCNIV 120
Db 28 POEVSYTDIVYINGSGGVVYQAKLCSGSELVAIKVLDQRFPKRELQIRKLDHCNIV 87
Qy 121 RLRYFFYSGEKKDEVLINLVLDVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLA 180
Db 88 RLRYFFYSGEKKDEVLINLVLDVPETVYRVARHYSRAKQTLPIVYKLYMYQLFRSLA 147
Qy 181 YIHSFGICHHDIRQNLLDPDPAVYKLCDFGSAKOLVRGEPNVSYICSHYYAPABELIFG 240
Db 148 YIHSFGICHHDIRQNLLDPDPAVYKLCDFGSAKOLVRGEPNVSYICSHYYAPABELIFG 207
Qy 241 ATDVTSSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQIIRKNNPNYTE 300
Db 208 ATDVTSSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQIIRKNNPNYTE 267
Qy 301 FKFPQIKAMPWTVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVK 360
Db 268 FKFPQIKAMPWTVFRPTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVK 327
Qy 361 PNGRDTALPNTTOELSSNPPLATILIPPHARI 394
Db 361 PNGRDTALPNTTOELSSNPPLATILIPPHARI 384

Db 328 PNGRDTPALFNFPTTQELSSNPPLATITLIPPHARI 361

RESULT 9
US-10-211-412B-3
Sequence 3, Application US/10211412B

Patent No. 6716624
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-412B-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.8e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 MEWPMEGGSGRRRTTSPAESCKPVQPSAFSGMSKSRDSDSKTTVVATPGCGDR 60
Db 1 MEWPMEGGSG-----GSKVTTVATPGCGDR 27
Qy 61 POEVSYDTTKYIGNSFGVYVQAKLDSGELVAIKVLQDKRFKRELOIMRKLDHCNIV 120
Db 28 POEVSYDTTKYIGNSFGVYVQAKLDSGELVAIKVLQDKRFKRELOIMRKLDHCNIV 87
Qy 121 RLRYFFSYSGEKQEVYINLVLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLA 180
Db 88 RLRYFFSYSGEKQEVYINLVLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLA 147
Qy 181 YHSGFGICHRDIKQPNLLDPTAVLKLCDFGSAKQIVRGEPNVSYSRYRAPELIFG 240
Db 148 YHSGFGICHRDIKQPNLLDPTAVLKLCDFGSAKQIVRGEPNVSYSRYRAPELIFG 207
Qy 241 ATDTTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIREMNPYTE 300
Db 208 ATDTTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIREMNPYTE 267
Qy 301 FKFPQIKAPMTKVFRRPTPEPAIALCSRLLGYPTARLTPLBACAHSPFDELDPNVKH 360
Db 268 FKFPQIKAPMTKVFRRPTPEPAIALCSRLLGYPTARLTPLBACAHSPFDELDPNVKH 327
Qy 361 PNGRDTPALFNFPTTQELSSNPPLATITLIPPHARI 394
Db 328 PNGRDTPALFNFPTTQELSSNPPLATITLIPPHARI 361

RESULT 10
US-09-916-109-5
Sequence 5, Application US/09916109
Patent No. 6465231
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang

APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-5

Query Match 77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.1e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGMSGRPRT-TSFAESCKPVQPSAFSGMSKSRDSDSKTTVVATPGCGDRPQEVSY 66
Db 73 GGGSGGPGAGTSFPP-----GVKLR--DSGKVTTVVATLGGCPERSQEVAY 119
Qy 67 TDTYVIGNSFGVYVQAKLDSGELVAIKVLQDKRFKRELOIMRKLDHCNIVRLRYFF 126
Db 120 TDIRYIGNSFGVYVQAKLDSGELVAIKVLQDKRFKRELOIMRKLDHCNIVRLRYFF 179
Qy 127 YSSGEKQEVYINLVLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFG 186
Db 180 YSSGEKQEVYINLVLDVYPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFG 239
Qy 187 ICHRDIKQPNLLDPTAVLKLCDFGSAKQIVRGEPNVSYSRYRAPELIFGATDYS 246
Db 240 VCHRDIKQPNLLDPTAVLKLCDFGSAKQIVRGEPNVSYSRYRAPELIFGATDYS 299
Qy 247 SIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIREMNPYTEKFPQI 306
Db 300 SIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIREMNPYTEKFPQI 359
Qy 307 KAHFMTKVFRRPTPEPAIALCSRLLGYPTARLTPLBACAHSPFDELDPNVKHNGRDT 366
Db 360 KAHFMTKVFRRPTPEPAIALCSRLLGYPTARLTPLBACAHSPFDELDPNVKH 419
Qy 367 PALFNFPTTQELSSNPPLATITLIPPHAR 393
Db 420 PALFNFPTTQELSSNPPLATITLIPPHAR 446

RESULT 11
US-10-211-412B-5
Sequence 5, Application US/10211412B
Patent No. 6716624
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/211,412B
CURRENT FILING DATE: 2002-07-31
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
TYPE: PRT

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: ORGANISM: Homo sapiens
US-10-211-412B-5

Query Match      77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6,1e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCKPVQPSAFGSMKVSBDKDGSKVTYVATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTYVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQAKRLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 239

Qy 187 ICHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 246
Db 240 VCHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 419

Qy 367 PALFNFTTOELSSNPPLATLILPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAILIPHLR 446

RESULT 12
US-09-916-109-4
: Sequence 4, Application US/09916109
: Patent No. 6465231
: GENERAL INFORMATION:
: APPLICANT: Harrison, Stephen D.
: APPLICANT: Calderon-Cacia, Maria
: APPLICANT: Calderon-Cacia, Maria
: APPLICANT: Zhong, Ziyang
: APPLICANT: Fang, Eric Y.
: APPLICANT: Colt, Doris G.
: APPLICANT: Nguyen, Steve H.
: APPLICANT: Medina-Selby, Angelica
: TITLE OF INVENTION: GSK3 POLYPEPTIDES
: FILE REFERENCE: PP-15876.002/200130.524
: CURRENT APPLICATION NUMBER: US/09/916,109
: CURRENT FILING DATE: 2001-07-25
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 483
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-916-109-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 6,9e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCKPVQPSAFGSMKVSBDKDGSKVTYVATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTYVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQAKRLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 239

Qy 187 ICHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 246
Db 240 VCHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 419

Qy 367 PALFNFTTOELSSNPPLATLILPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAILIPHLR 446
```

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Qy 127 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 239

Qy 187 ICHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 246
Db 240 VCHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 419

RESULT 13
US-10-211-412B-4
: Sequence 4, Application US/10211412B
: Patent No. 6716624
: GENERAL INFORMATION:
: APPLICANT: Harrison, Stephen D.
: APPLICANT: Hall, John A.
: APPLICANT: Calderon-Cacia, Maria
: APPLICANT: Zhong, Ziyang
: APPLICANT: Fang, Eric Y.
: APPLICANT: Colt, Doris G.
: APPLICANT: Nguyen, Steve H.
: APPLICANT: Medina-Selby, Angelica
: TITLE OF INVENTION: GSK3 POLYPEPTIDES
: FILE REFERENCE: 59516-162/PP-15876.002/200130.524
: CURRENT APPLICATION NUMBER: US/10/211,412B
: CURRENT FILING DATE: 2002-07-31
: PRIOR APPLICATION NUMBER: US09/916,109
: PRIOR FILING DATE: 2001-07-25
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 483
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-211-412B-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 6,9e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCKPVQPSAFGSMKVSBDKDGSKVTYVATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTYVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQAKRLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYVNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 239

Qy 187 ICHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSFG 246
Db 240 VCHRDIPKQNLVLDYVPEYTVRVARHYSRAKOTLPVLYVYLWYQLFRSLAYIHSOG 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPYTEFKEPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLACAHSPFDELDPNVKHPNGRDT 419
```

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Db      360 KAHPTKTFKSTPPEALALCSSLEETPSSRLSFLCACAHFPDELRCLGTQLPNNRPL 419
      367 PALFNFTTOELSSNPPLATILIPPHAR 393
      420 PPLFNFSAGELSLIOPSLNAILIPPHLR 446
```

RESULT 14

```
US-09-538-092-1162
; Sequence 1162, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Manifest, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1162
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49840
US-09-538-092-1162
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Query Match 77.3%; Score 1609; DB 2; Length 483;

Best Local Similarity 80.6%; Pred. No. 6,9e-169;

Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

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Qy      8 GCGSGMRPRT-TSFAESCKPVQPSAFGSMKVSRLDKSGKVTTVVATPQGGPRPOEVSX 66
Db      73 GCGSGGAGTGFSPRP-----GVKLGR--DSGKVTTVATLGGGPERGQVAY 119
Qy      67 TDTKVIKNGSGFVYQAKLQDSGELVAIKVLODYRFKRRLEQIRKLDHCNIVRLRYFF 126
Db      120 TDIKVIKNGSGFVYQARLAETRELVAIKVKVQDGRFKRRLEQIRKLDHCNIVRLRYFF 179
Qy      127 YSSGSKDEYVNLVLDVPEETVYVARHYSRAKOTLPVIVKLYMYQLFRSLAYIHSFG 186
Db      180 YSSGSKDELYNLVLEVPETVYVARHFTAKLTLPILVYKVMYQLFRSLAYIHSOG 239
Qy      187 ICHRDIKPQNLILDDPTAVLKLCDFGSAKQLVGRSPNYSICSRYYRAPELIFGATDYTS 246
Db      240 VCHRIKQNLILVDDPTAVLKLCDFGSAKQLVGRSPNYSICSRYYRAPELIFGATDYTS 299
Qy      247 SIDVMSACVLAELLIGQPIFGDSGVQDVEIIVLGTPTREQIREMNPNTFEKFPQI 306
Db      300 SIDVMSACVLAELLIGQPIFGDSGVQDVEIIVLGTPTREQIREMNPNTFEKFPQI 359
Qy      307 KAHPTKTFKSTPPEALALCSSRLLEYPTATLTLELACAHSPDELRDPNVKHXNGRDT 366
Db      360 KAHPTKTFKSTPPEALALCSSRLLEYPTSSRLSPLACAHSPFDELRCLGTQLPNNRPL 419
Qy      367 PALFNFTTOELSSNPPLATILIPPHAR 393
Db      420 PPLFNFSAGELSLIOPSLNAILIPPHLR 446
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RESULT 15

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US-09-916-109-7
; Sequence 7, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
```

```
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacila, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-7
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Query Match 76.3%; Score 1588; DB 2; Length 351;

Best Local Similarity 86.2%; Pred. No. 8.6e-167;

Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

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Qy      46 KVTTVVATPQGGPRPOEVSYTDPTKVIKNGSGFVYQAKLQDSGELVAIKVKLODKRFKN 105
Db      3 KVTTVVATLGGGPERGQVAYTDIKVIGNSFGVYQARLAETRELVAIKVKLODKRFKN 62
Qy      106 RELQIMRKLDHCNIVRLRYFFYSSGSKDEYVNLVLDVPEETVYVARHYSRAKOTLPV 165
Db      63 RELQIMRKLDHCNIVRLRYFFYSSGSKDELYNLVLEVPETVYVARHFTAKLTPI 122
Qy      166 IYVKLYMYQLFRSLAYIHSFGICHRDIPQNLILDDPTAVLKLCDFGSAKQLVGRSPNV 225
Db      123 LVYKVMYQLFRSLAYIHSOGVCHRDIPQNLVDDPTAVLKLCDFGSAKQLVGRSPNV 182
Qy      226 YICSRYYRAPELIFGATDYTSIDVMSAGCYLAELLIGQPIFGDSGVQDVEIIVKLTGT 285
Db      183 YICSRYYRAPELIFGATDYTSIDVMSAGCYLAELLIGQPIFGDSGVQDVEIIVKLTGT 242
Qy      286 PTRQIREMNPNTFEKFPQIKAHPTKVFRRPTPPEALALCSSRLLEYPTATLTPLFLAC 345
Db      243 PTRQIREMNPNTFEKFPQIKAHPTKVFRRPTPPEALALCSSRLLEYPTSSRLSPLFLAC 302
Qy      346 AHSFPDELRDPNVKHXNGRDTPALFNFTTOELSSNPPLATILIPPHAR 393
Db      303 AHSFPDELRCLGTQLPNNRPLPPLFNFSAGELSLIOPSLNAILIPPHLR 350
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Search completed: May 16, 2006, 15:11:10

Job time : 46 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2006, 15:05:56 ; Search time 41 Seconds
(without alignments)
924.620 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081
Sequence: 1 MEWPMEGGMSGRPTTSF.....OELSNPLPATLLPPIHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.80:*
1: Dairl:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2024 | 97.3 | 420 | 1 | glycogen synthase |
| 2 | 2010 | 96.6 | 420 | 1 | tau-protein kinase |
| 3 | 1931 | 92.8 | 420 | 2 | intracellular kina |
| 4 | 1923 | 92.4 | 420 | 2 | glycogen synthase |
| 5 | 1607 | 77.2 | 483 | 1 | protein kinase (EC |
| 6 | 1590.5 | 76.4 | 575 | 2 | protein kinase egg |
| 7 | 1542.5 | 74.1 | 733 | 2 | probable protein k |
| 8 | 1542.5 | 74.1 | 1067 | 2 | protein kinase seg |
| 9 | 1342.5 | 64.5 | 362 | 2 | hypothetical prote |
| 10 | 1296 | 62.3 | 409 | 2 | shaggy protein kin |
| 11 | 1275.5 | 61.3 | 471 | 2 | shaggy protein kin |
| 12 | 1273.5 | 61.2 | 471 | 1 | shaggy protein kin |
| 13 | 1265 | 60.8 | 408 | 2 | shaggy protein kin |
| 14 | 1258 | 60.5 | 472 | 1 | serine/threonine-s |
| 15 | 1256 | 60.4 | 412 | 1 | protein kinase MSK |
| 16 | 1249 | 60.0 | 403 | 2 | probable shaggy-1 |
| 17 | 1249 | 60.0 | 431 | 2 | shaggy protein kin |
| 18 | 1247.5 | 59.9 | 469 | 1 | shaggy protein kin |
| 19 | 1246 | 59.9 | 409 | 1 | protein kinase ASK |
| 20 | 1245 | 59.8 | 412 | 2 | shaggy-like protei |
| 21 | 1244 | 59.8 | 411 | 1 | tau-protein kinase |
| 22 | 1239 | 59.5 | 409 | 2 | shaggy-like protei |
| 23 | 1234 | 58.3 | 380 | 2 | tau-protein kinase |
| 24 | 1233 | 58.3 | 412 | 2 | shaggy-like protei |
| 25 | 1232 | 59.2 | 405 | 1 | probable shaggy-1 |
| 26 | 1232 | 59.2 | 407 | 2 | shaggy-like protei |
| 27 | 1229.5 | 59.1 | 420 | 2 | probable glycogen |
| 28 | 1229.5 | 59.1 | 469 | 1 | shaggy protein kin |
| 29 | 1228.5 | 59.0 | 447 | 2 | hypothetical prote |

| | | | | | |
|----|--------|------|-----|---|--------|
| 30 | 1226 | 58.9 | 411 | 1 | 537644 |
| 31 | 1226 | 58.9 | 468 | 2 | 708139 |
| 32 | 1220 | 58.6 | 421 | 2 | S51938 |
| 33 | 1208 | 58.0 | 447 | 2 | T01756 |
| 34 | 1178 | 56.6 | 468 | 2 | A5476 |
| 35 | 1158 | 55.6 | 431 | 2 | T47908 |
| 36 | 1156.5 | 55.6 | 387 | 2 | T37758 |
| 37 | 1109.5 | 53.3 | 354 | 2 | T45138 |
| 38 | 996 | 47.9 | 381 | 2 | T40746 |
| 39 | 996 | 47.9 | 390 | 2 | T43008 |
| 40 | 978.5 | 47.0 | 452 | 2 | T18457 |
| 41 | 940.5 | 45.2 | 354 | 2 | F90121 |
| 42 | 940 | 45.2 | 370 | 2 | A63447 |
| 43 | 873.5 | 42.0 | 501 | 2 | S67615 |
| 44 | 792 | 38.1 | 211 | 2 | T04119 |
| 45 | 735.5 | 35.3 | 367 | 2 | T19937 |

ALIGNMENTS

RESULT 1
S53324
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S53324
R:Stambolic, V.; Woodgett, J.R.
Biochem. J. 303, 701-704, 1994
A:Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via ser
A:Reference number: S53324; MUID:95071278; PMID:7980435
A:Accession: S53324
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-420 <STA>
A:Cross-references: UNIPROT:P49841; UNIPARC:UPI00004893D; EMBL:L33801; NID:9529236; PID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (see
C:Genetics:
A:Gene: GDB:GSK3B
A:Cross-references: GDB:6108057
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status ex
F:85/Active site: Lys #status predicted

Query Match 97.3%; Score 2024; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-89;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 11 | MSGRPTTSFASCKPVOQPSAFSGMKVSRKDDSKYTTVAATPQGGPDRPOEVSYTQK | 70 |
| DB | 1 | MSGRPTTSFASCKPVOQPSAFSGMKVSRKDDSKYTTVAATPQGGPDRPOEVSYTQK | 60 |
| QY | 71 | VINGSGFQVNVQAKLCDSGELVAIKVQLQDRFPKRLQIRKLDHCNIVLRFFYSSG | 130 |
| DB | 61 | VINGSGFQVNVQAKLCDSGELVAIKVQLQDRFPKRLQIRKLDHCNIVLRFFYSSG | 120 |
| QY | 131 | EKQDEVYINLVLDVPEPVVVAHYSRAKTLVYIYKLYMQLFRSLAYIHSFGICHR | 190 |
| DB | 121 | EKQDEVYINLVLDVPEPVVVAHYSRAKTLVYIYKLYMQLFRSLAYIHSFGICHR | 180 |
| QY | 191 | DIKFQNLIDPDTVAIVLKCDPSAKOLVRGEPNYSICSRYYRAPELLFGATDYSIDV | 250 |
| DB | 181 | DIKFQNLIDPDTVAIVLKCDPSAKOLVRGEPNYSICSRYYRAPELLFGATDYSIDV | 240 |
| QY | 251 | WSACCVLAELLAGPIFFGDSGVQDLVEIIVKLGTPTRBOQIRENNPNYTEKFPQIKAP | 310 |
| DB | 241 | WSACCVLAELLAGPIFFGDSGVQDLVEIIVKLGTPTRBOQIRENNPNYTEKFPQIKAP | 300 |
| QY | 311 | WTKVFRPTTPPBALALCSRLLETTPTARLTPLKCAHSFDELDPNVAKHNGRDTPLAF | 370 |

```
Db 301 WTKVFRRTPEPALALCSRLLEVTPTARLTPLLEACAHSPFDELDPNVKHNKGDTPLAF 360
Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 2
TVRTKB
tau-protein kinase (EC 2.7.1.135) I - rat
N:Alternate names: factor A/ glycogen synthase kinase 3 beta; protein kinase GSK-3-beta;
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S14708; S33741; S36723
R:Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A:Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A:Reference number: S14707; MUID:90316097; PMID:2164470
A:Accession: S14708
A:Molecule type: mRNA
A:Residues: 1-420 <WOO>
A:CROSS-references: UNIPROT:P18266; UNIPARC:UPI000012DDC0; EMBL:X53428; NID:956333; PIDN
A:Note: the author translated the codon ATG for residue 240 as Val
R:Ichiguro, K.; Shiratsuchi, A.; Sato, S.; Omori, A.; Arioka, M.; Kobayashi, S.; Uchida,
FEBS Lett. 325, 167-172, 1993
A:Title: Glycogen synthase kinase 3-beta is identical to tau protein kinase I generating
A:Reference number: S33741; MUID:93307488; PMID:7686508
A:Accession: S33741
A:Molecule type: mRNA
A:Residues: 1-239, 'V', 241-420 <ISH>
A:CROSS-references: UNIPARC:UPI00000018B4; EMBL:X73653; NID:g402651; PIDN:CAA52020.1; PI
A:Accession: S36729
A:Molecule type: protein
A:Residues: 37-58; 61-74; 151-158; 293-316; 318-325; 327-332; 351-368; 370-375 <ISH2>
A:CROSS-references: UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538;
S3D
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:85/Active site: Lys #status predicted

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
I51425
intracellular kinase (EC 2.7.1.-) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51425
R:Pierce, S.B.; Kimmel, D.
Development 121, 755-765, 1995
A:Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A:Reference number: I51425; MUID:95237008; PMID:7720580
A:Accession: I51425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-420 <PIE>
A:CROSS-references: UNIPROT:Q91757; UNIPARC:UPI00000F8682; GB:L38492; NID:g727189; PIDN:J
C:Genetics:
A:Gene: Xgsk-3
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:85/Active site: Lys #status predicted

Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 6.5e-85;
Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
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```
Qy 11 MSGRPRTTSPAESCKPVQQPSAFSGSMKVSRLDKSGSKYTTVATPGQSPDRPOEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFSGSMKVSRLDKSGSKYTTVATPGQSPDRPOEVSYTDTK 60
Qy 71 VINGSGFVVYQAKLCSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRFFYSYG 130
Db 61 VINGSGFVVYQAKLCSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRFFYSYG 120
Qy 131 EKDEYVNLVLDVPEPTVTVARHVSRAQALPIIVKLYMQLFSLAYIHSGFCH 190
Db 121 EKDEYVNLVLDVPEPTVTVARHVSRAQALPIIVKLYMQLFSLAYIHSGFCH 180
Qy 191 DIKQNLDPDPTAVLKLCSGSAKQIVRGSPNVSYICSRYYRAPELIFGATDTSIDV 250
Db 181 DIKQNLDPDPTAVLKLCSGSAKQIVRGSPNVSYICSRYYRAPELIFGATDTSIDV 240
Qy 251 WSACCVLAELLQPIFGDSDVDQVLEIKVLTGPTREQIREMNPYTEFKEPQIKAH 310
Db 241 WSACCVLAELLQPIFGDSDVDQVLEIKVLTGPTREQIREMNPYTEFKEPQIKAH 300
Qy 311 WTKVFRRTPEPALALCSRLLEVTPTARLTPLLEACAHSPFDELDPNVKHNKGDTPLAF 370
Db 301 WTKVFRRTPEPALALCSRLLEVTPTARLTPLLEACAHSPFDELDPNVKHNKGDTPLAF 360
Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4
I51692
glycogen synthase kinase (EC 2.7.1.-) 3 beta - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51692
R:Dominguez, I.; Itoh, K.; Sokol, S.Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 8498-8502, 1995
A:Title: Role of glycogen synthase kinase 3 beta as a negative regulator of dorsoventral
A:Reference number: I51692; MUID:95356823; PMID:7667318
A:Accession: I51692
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-420 <DOM>
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A:Cross-references: UNIPROT:Q91627; UNIPARC:UPI000006B97; EMBL:U1862; NID:g1000734; PDB:1A862
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP, phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:85/Active site: Lys #status predicted

Query Match 92.4%; Score 1923; DB 2; Length 420;
Beet Local Similarity 95.0%; Pred. No. 1.6e-84;
Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 11 MSGRRITTSFASCPVQOPSAFGSMKVSRLDKSGSKTTVVATPGQSPDRPOEVSYTDTK 70
DB 1 MSGRRITTSFASCPVQOPSAFGSMKVSRLDKSGSKTTVVATPGQSPDRPOEVSYTDTK 60
QY 71 VIINGSFGVYQAKLCDGELVAIKKVLQDKKFKNRELQIMKLDHCNIVRLRYFFYS 130
DB 61 VIINGSFGVYQAKLCDGELVAIKKVPQDKFKNRELQIMKLDHCNIVRLRYFFYS 120
QY 131 EKKDEVYLNLYVDYPERYVARRHYRAKQTLPIYVYKLYMQLFRSLAYTHSGICHR 190
DB 121 EKKDEVYLNLYVDYPERYVARRHYRAKQALPIYVYKLYMQLFRSLAYTHSGICHR 180
QY 191 DIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYSRYYRADELIFGATDYTSIDV 250
DB 181 DIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYSRYYRADELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQIPFGDSVDQLVEIILKVLGTPTRBOIRKMNPNYTEFKPQIKAMP 310
DB 241 WSAGCVLAELLGQIPFGDSVDQLVEIILKVLGTPTRBOIRKMNPNYTEFKPQIKAMP 300
QY 311 WTKVRRPTPPPAALICSRILEYTPARLTPLCAHNSFDELDRPNVAKHPNGRPTPALF 370
DB 301 WTKVRRPTPPPAALICSRILEYTPARLTPLCAHNSFDELDRPNVAKHPNGRPTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHAR 393
DB 361 NPTTOELSSNPPLATILIPPHAR 383

RESULT 5

TVRTKA
protein kinase (EC 2.7.1.37) GSK-3-alpha - rat
N:Alternate names: factor A; glycogen synthase kinase 3 alpha
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
A:Accession: S14707
R:Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A:Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A:Reference number: S14707; MUID:90316097; PMID:2164470
A:Accession: S14707
A:Molecule type: mRNA
A:Residues: 1-483 <RNA>
A:Cross-references: UNIPROT:P18265; UNIPARC:UPI000012DDBF; EMBL:X53427; NID:g56331; PIDN:CA50215.1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP, phosphoprotein, phosphotransferase; serine/threonine-specific protein kinase
F:117-378/Domain: protein kinase homology <KIN>
F:112-133/Region: protein kinase ATP-binding motif
F:148/Active site: Lys #status predicted

Query Match 77.2%; Score 1607; DB 1; Length 483;
Beet Local Similarity 80.6%; Pred. No. 1.6e-69;
Matches 312; Conservative 23; Mismatches 38; Indels 14; Gaps 3;

QY 8 GGGGSGRRRT-TSFASCKPVQOPSAFGSMKVSRLDKSGSKTTVVATPGQSPDRPOEVS 66
DB 73 GGGGSGRRRT-TSFASCKPVQOPSAFGSMKVSRLDKSGSKTTVVATPGQSPDRPOEVS 66
QY 67 TDTKVIINGSFGVYQAKLCDGELVAIKKVLQDKKFKNRELQIMKLDHCNIVRLRYFF 126
DB 120 TDTKVIINGSFGVYQAKLCDGELVAIKKVLQDKKFKNRELQIMKLDHCNIVRLRYFF 179

QY 127 YSSGKKDEVYLNLYVDYPERYVARRHYRAKQTLPIYVYKLYMQLFRSLAYTHSG 186
DB 180 YSSGKKDEVYLNLYVDYPERYVARRHYRAKQTLPIYVYKLYMQLFRSLAYTHSG 239
QY 187 ICHRDIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYSRYYRADELIFGATDYTS 246
DB 240 ICHRDIKPNLLDPTAVLKLCDFGSAKQLVGEPNVSYSRYYRADELIFGATDYTS 299
QY 247 SIDWSAGCVLAELLGQIPFGDSVDQLVEIILKVLGTPTRBOIRKMNPNYTEFKPQI 306
DB 300 SIDWSAGCVLAELLGQIPFGDSVDQLVEIILKVLGTPTRBOIRKMNPNYTEFKPQI 359
QY 307 KAHPTKVRPTPPPAALICSRILEYTPARLTPLCAHNSFDELDRPNVAKHPNGRDT 366
DB 360 KAHPTKVRPTPPPAALICSRILEYTPARLTPLCAHNSFDELDRPNVAKHPNGRDT 419
QY 367 PALFNTTOELSSNPPLATILIPPHAR 393
DB 420 PALFNTTOELSSNPPLATILIPPHAR 446

RESULT 6

S35327
protein kinase egg39 (EC 2.7.1.-) (clone pNB39) - fruit fly (Drosophila melanogaster)
N:Alternate names: zw3-A
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
A:Accession: S35327; S35326; S35329; A44331; S16691; S35421; S35422; S35424
R:Ruel, L.; Parlesco, V.; Lutz, Y.; Simpson, P.; Boutrouls, M.
EMBO J. 12, 1657-1669, 1993

A:Title: Functional significance of a family of protein kinases encoded at the shaggy 10
A:Reference number: S35325; MUID:93223707; PMID:8467811
A:Accession: S35327
A:Molecule type: mRNA

A:Residues: 1-575 <RUB>
A:Cross-references: UNIPROT:P18431; UNIPARC:UPI00002B384; EMBL:X70863; NID:g11145; PIDN:CA50215.1

A:Accession: S35326
A:Molecule type: mRNA
A:Residues: 1-196; 'R', 198-394; 'D', 396-512; 'D', 514 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6A; EMBL:X70862; NID:g11143; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

A:Accession: S35329
A:Molecule type: mRNA
A:Residues: 1-42 <RUB>
A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PIDN:CA50215.1

C:GeneticCB:
A:Gene: FlyBase:egg
A:Cross-references: FlyBase:FBgn000371
C:Keywords: alternative splicing; ATP; phosphoprotein; phototransferase; serine/threonine kinase F52-313/Domains protein kinase homology <Kin>
F60-68/Region: protein kinase ATP-binding motif

Query Match 76.4%; Score 1590.5; DB 2; Length 575;
Best Local Similarity 79.6%; Pred. No. 1.le-68;
Matches 305; Conservative 32; Mismatches 41; Indels 5; Gaps 4;

Dy 11 MSGRPTTSFAESCKPVQPS-AFGSMKVSNDXGSKVTTVATPGGPDRPOEVSTDT 69
|||:|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MSGRPTTSSFAEGNK--QSPLVLGVVTC-SRGSKITTVAVTPGGCTDVGQSVSYTD 57

Oy 70 KVIINGSGVVYQAOKLCDSGELVAIKYLADRRKENBELQIMRLDHNCIYRLFYEFS 129
Db 58 KVINGSGVVYFOAKLCDTGELVAIKYLADRKKNELQMRLLENHNYKLKYFYESS 117

Oy 130 GEKDDEVNLIVLDVPETVTVARAHYSRAKOTLPVITYKLWYOLESFLAYHSFGICH 189
Db 118 GEKDDEVALNILEVIPETVTVVARQYAKTKQTIPINERILMYQLFRSLAYHSLSIGH 177

Oy 190 RDIKPQNLLDPRTAVLYCLDFGSAGOLVREEPNVSYCSRYAPAELEIFPATDYTSID 249
Db 178 RDIRPQNLLDPETAVALVLCDFGSAGOLMHEPNVSYCSRYPARELIFFAINYTVID 237

Oy 250 VMSAGCVLAELLGOPIFPDGSDVDLVIEIKVIGTFPREQIREMPVYTEFKFPQIAH 309
Db 238 VMASGCUALLELLGOPIFPDGSDVDLVIEIKVIGTFPREQIREMPVYTEFKFPQISK 297

Oy 310 PMTKVFPRTRPEPAIALCSRLLEYTPTRLPLECAHSFFDEL-R-DENVKHNGRDTPA 368
Db 298 PMQKVPRTRTEBAINILVSLLETTPSARIITPLACAFPFEDLRMEGNHTLPMGRMBP 357

Oy 369 LFNFTTELSSNPPLATTILLPPH 391
Db 358 LFNFTEHELSTQPISLVPLLPH 380

RESULT 7
S10932
Probable protein kinase zeste-white3 (EC 2.7.1.-) (clone cKZ5) - fruit fly (*Drosophila melanogaster*)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C:Accession: S10932
R:Siegfried, E.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.
A>Title: Putative protein kinase product of the *Drosophila* segment-polarity gene *zeste-white3*.
A:Reference number: S10931; PMID:90294930; PMID:2113617
A:Accession: S10932
A:Molecule type: mRNA
A:Residues: 1..733 <SITE>
A:CROSS-references: UNIPARC:UPI000016BE18; EMBL:X54006; NID:g8857; PIDD:CAA37952.1; PID:F52-313/
A:Note: It is uncertain whether Met-1 or Met-44 is the initiator or whether translation C/Genetics: A:Gene: zw3
A:CROSS-references: FlyBase:FBgn000371
C:Keywords: alternative splicing; ATP; phosphoprotein; phototransferase; serine/threonine kinase F52-313/Domains protein kinase homology <Kin>
F60-68/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 733;
Best Local Similarity 75.9%; Pred. No. 2.5e-66;
Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

Oy 7 EGCGMSGRPRTTSFAESC---KEVOQSFASFMSMKVRDKDSKITTTVAATPGGPDRPQ 62
|||:|||::|||::|||::|||::|||::|||::|||::|||
Db 230 DGSEENVKTAATARTGTSCSVSWTYVK-----PKNILGRGSKIITTVATPGGCTRIVQ 283
EVSYYTDKVIANGSPGVVYAOKLCDSELVAIKYLADRRKNELQIMRLDHNCIYRLF 122

Db EVSYDTKVIINGSGGVVFOALCTDGLGELVAIKVLQDRFKFKRELQIMKLEHCNIYKL 343
 QY 123 RYFFYSGGKKOEYVNLVLDVPETVYVRAHRYBSAKQTLPVLYVQLYVQLEFRSLAYI 182
 Db 344 LYFFYSGGKKRDEVELNLVLEYIPETVYVKAQYAKTKQTIPINFLVYVQLFRSLAYI 403
 QY 183 HSFGLCHRDIKQNLLDPTAVLKLCDFGSAQQLVGRGENNVYICGRYRAPAPLIGAT 242
 Db 404 HSLGICHRDIKQNLLDPTAVLKLCDFGSAQQLHGEENNVYICGRYRAPAPLIGAI 463
 QY 243 DYTSSIDVWSAGCVLAELLGGPIFPDGSVDQVLEIIKVLGTPTRQIREMNNYIEFK 302
 Db 464 NNTTKIDVWSAGCVLAELLGGPIFPDGSVDQVLEIVIKVLGTPTRQIREMNNYIEFK 523
 QY 303 FPOIKAHPTKVFRRPPTPEAIALCSRLLEYTPALTPLEACAHSEFDELRLDPNVKHP 361
 Db 524 FPOIKSHPWQKVFRRTPTEALINVLSELYTESAITPLKACAHPEFDELRLMEGNHTLP 583
 QY 362 NGRDTPALPFTTQELSSNPPLATILIPPH 391
 Db 584 NGRDMPPLPFTPEHELSIQSLVLPQLLPKH 613

RESULT 8
 S35423 protein kinase egg46 (EC 2.7.1.-) - fruit fly (*Drosophila melanogaster*)
 C|Species: *Drosophila melanogaster*
 C|date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
 C|Accession: S35328; S35423
 R|Ruel, L.; Pantescio, V.; Lutz, Y.; Simpson, P.; Bourouis, M.
 EMBL J. 12, 1657-1659, 1993
 A|Title: Functional significance of a family of protein kinases encoded at the shaggy loci
 A|Reference number: S35325; MUID:93223707; PMID:8467811
 A|Accession: S35328
 A|Status: preliminary
 A|Molecule type: mRNA
 A|Residues: 1-1067 <RUE>
 A|Cross-references: UNIPARC:UPI00013591B; EMBL:X70864; NID:G11147; PIDN:CAA50214.1; PID
 C|Genetics:
 A|Gene: FlyBase:egg
 A|Cross-references: FlyBase:FBgn0003371
 C|Keywords: ATP; phosphotransferase
 F|605-866/Domain: protein kinase homology <KIN>
 F|613-621/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 1067;
 Best local similarity 75.9%; Pred. No. 3.5e-66;
 Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

QY 7 EGGKNSGRPRITTSFAESC-----KPVQPSAFSGSMKYSRDKGSKYTTVATPGGSPDRPQ 62
 Db 550 DQSGENVATKAKLARTQSCVSWTKVQK-----FNKILGRDGSKITTVATPGGSDRVQ 603
 QY 63 EVSYDTKVIINGSGGVVFOALCTDGLGELVAIKVLQDRFKFKRELQIMKLEHCNIYVL 122
 Db 604 EVSYDTKVIINGSGGVVFOAKLCTDGLGELVAIKVQLQDRFKFKRELQIMKLEHCNIYKL 663
 QY 123 RYFFYSGGKKOEYVNLVLDVPETVYVRAHRYBSAKQTLPVLYVQLYVQLEFRSLAYI 182
 Db 664 LYFFYSGGKKRDEVELNLVLEYIPETVYVKAQYAKTKQTIPINFLVYVQLFRSLAYI 723
 QY 183 HSFGLCHRDIKQNLLDPTAVLKLCDFGSAQQLVGRGENNVYICGRYRAPAPLIGAT 242
 Db 724 HSLGICHRDIKQNLLDPTAVLKLCDFGSAQQLHGEENNVYICGRYRAPAPLIGAI 783
 QY 243 DYTSSIDVWSAGCVLAELLGGPIFPDGSVDQVLEIIKVLGTPTRQIREMNNYIEFK 302
 Db 784 NNTTKIDVWSAGCVLAELLGGPIFPDGSVDQVLEIVIKVLGTPTRQIREMNNYIEFK 843
 QY 303 FPOIKAHPTKVFRRPPTPEAIALCSRLLEYTPALTPLEACAHSEFDELRLDPNVKHP 361
 Db 844 FPOIKSHPWQKVFRRTPTEALINVLSELYTESAITPLKACAHPEFDELRLMEGNHTLP 903

A:Residues: 1-472 <GB1>
 A:Cross-references: UNIPROT:Q96287; UNIPARC:UPI000000005CA; EMBL:AF058919; NID:G3047100;
 C:Genetics:
 A:Gene: ATSP:FN23.11
 A:Map position: 5
 A:Introns: 21/3; 103/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 385/3; 413/3; 4
 C:Superfamily: kinase-related transforming protein; protein kinase
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:136-397/Domain: protein kinase homology <kin>
 F:144-152/Region: protein kinase ATP-binding motif
 F:167/Active site: Lys #status predicted

Query Match 60.4%; Score 1258; DB 1; Length 472;
 Best Local Similarity 61.6%; Pred. No. 5e-53;
 Matches 250; Conservative 54; Mismatches 74; Indels 28; Gaps 9;

Qy 10 GMSGRPTTSPAESCKPV---QPSAFGSMKV-----SRDKD-----GSKVTTV 51
 Db 67 GTSNVP-----AVSKRPDDQLPDVMIEKIRDEGNAREDKDMETTVVNSGTETGVYI 121
 Qy 52 ATPGGPDRP-QEVSYDTKVIKNGSGVYVQAKLCSGELVAIKVQLQDKRFKURELQ 109
 Db 122 TTVVGGRGDKPKQTISYMAQRVGTSFGVVFQAKCLETGEQVAIKVQLQDKRYKURELQ 181
 Qy 110 IMRKLDHCNIVALRYEFYSSGSEKDEYVNLVLDYVPETVVARHYSRAKQTLPIVYVK 169
 Db 182 IMRLQDHNPNVNLRRSFFSTTD-KDELVLNVLLEYVPEVTVRASRKYTKMNMHPITFVQ 240
 Qy 170 LYMVQLFSLAYIHS-FGICHRDIKQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYIC 228
 Db 241 LYTVCICALNVLHNVGVGCHRDIKPQNLVNPQTHQKICDFGSAKMLVPGEPNISTYC 300
 Qy 229 SRYRABELIFGATDYTSIDVWSAGCVLAELLGQPIFGSDGVQDVEIKVLGTPTR 288
 Db 301 SRYRABELIFGATEYTNADIMWSGCVVAELLGQPLFGESGIDQVLEIKVLGTPTR 360
 Qy 289 EQIREMNPVYTFEKKFPOIKAHFWTVFRPRTPPEAIALCSRLLEYTPARLTPLEACAH 348
 Db 361 EIRKCNPNYTFEKKFPOIKAHFWTKI FHKRMPEAVDLVSRLLQYSFNLCTALBACAH 420
 Qy 349 FDELDRPNVKHPNGRDTPALFNFPTTOELSSNP-PLATILLIPPHAR 393
 Db 421 FPDLDLRDENVSLPNGRALPLFNFPTTOELAGASTELRQRLIPAHQ 466

RESULT 15

S37642
 C:Species: Medicago sativa (alfalfa)
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: S37642
 R:Pay, A.; Jonak, C.; Boegre, L.; Mesiklene, I.; Mairinger, T.; Szalay, A.; Heberle-Bors,
 Plant J. 3, 847-856, 1993
 A:Title: The Mek family of alfalfa protein kinase genes encodes homologues of shaggy/Slx
 A:Reference number: S37642; MUID:94004996; PMID:8401615
 A:Accession: S37642
 A:Molecule type: mRNA
 A:Residues: 1-412 <PAY>
 A:Cross-references: UNIPARC:UPI000016D9F3; EMBL:X68409; NID:G31147; PIDN:CAA48472.1; PI
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:73-334/Domain: protein kinase homology <kin>
 F:81-89/Region: protein kinase ATP-binding motif
 F:104/Active site: Lys #status predicted

Query Match 60.4%; Score 1256; DB 1; Length 412;
 Best Local Similarity 61.2%; Pred. No. 5.5e-53;
 Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

Qy 6 MEGGMSGRPTTSPAESCKPV---QPSAFGSMKVSRDK-----DGSKVT---VV 51
 Db 2 MASGGVA--PASGFIDKXASSVGVKLPBEMNDMKIRDDKEMEAATYVDGNGTETGHITV 59

Qy 52 ATPGGPDRP-QEVSYDTKVIKNGSGVYVQAKLCSGELVAIKVQLQDKRFKURELQ 110
 Db 60 TTIGKNGQPKQTISYMAERVGHSGFVVFQAKCLETGEVVAIKVQLQDKRYKURELQ 119
 Qy 111 MRKLDHCNIVALRYEFYSSGSEKDEYVNLVLDYVPETVVARHYSRAKQTLPIVYVK 170
 Db 120 MRLLDHPNVSLKCFPSTTE-KDELVLNVLLEYVPEVTVSRVIRHYNQMNMHPITVYKL 178
 Qy 171 YMYQLFSLAYIHS-FGICHRDIKQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYICS 229
 Db 179 YSYQICRALAYIHSIGVCHRDIKQNLVNPHTHQLKICDFGSAKVLVKGEPNISTYCS 238
 Qy 230 RYRABELIFGATDYTSIDVWSAGCVLAELLGQPIFGSDGVQDVEIKVLGTPTR 289
 Db 239 RYRABELIFGATEYTNADIMWSAGCVLELLGQPLFGESGVDQVLEIKVLGTPTR 298
 Qy 290 QIREMNPVYTFEKKFPOIKAHFWTVFRPRTPPEAIALCSRLLEYTPARLTPLEACAH 349
 Db 299 EIKCNPNYTFEKKFPOIKAHFWTKI FHKRMPEAVDLVSRLLQYSFNLCTALBACAH 358
 Qy 350 FDELDRPNVKHPNGRDTPALFNFPTTOELSSNP-PLATILLIPPHAR 393
 Db 359 YDVRDPTTRLPNGRFLPFLFNFKVNEIKGVPAEMLVQLVPPHAR 403

Search completed: May 16, 2006, 15:10:18
 Job time : 42 secs

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OM protein - protein search, using sw model1

Run on: May 16, 2006, 15:02:06 ; Search time 185 Seconds
(without alignments)
935.758 Million cell updates/sec

Title: US-10-689-461-2
Perfect score: 2081
Sequence: 1 MEVMPMEGCGSGRPRRTSF.....QELSSNPPLATILIPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 2081 | 100.0 | 394 | 5 ABB07578 | ABD07578 Human trn |
| 2 | 2024 | 97.3 | 420 | 4 AAE05998 | Aae05998 Human gly |
| 3 | 2024 | 97.3 | 420 | 5 ABB07577 | ABD07577 Human gly |
| 4 | 2024 | 97.3 | 420 | 7 ABR44294 | ABr44294 Human gly |
| 5 | 2024 | 97.3 | 420 | 7 ADK11467 | AdK11467 Human gly |
| 6 | 2024 | 97.3 | 420 | 8 ADH09637 | AdH09637 Human hos |
| 7 | 2024 | 97.3 | 420 | 8 ADR40191 | Adr40191 Human gly |
| 8 | 2024 | 97.3 | 420 | 8 ADS92965 | AdS92965 Glycogen |
| 9 | 2024 | 97.3 | 420 | 8 ADT92555 | Adt92555 Human gly |
| 10 | 2013 | 96.7 | 414 | 8 ADR06333 | Adr06333 p38-alpha |
| 11 | 2013 | 96.7 | 420 | 2 AAR61327 | Aar61327 Tau-prote |
| 12 | 2013 | 96.7 | 420 | 5 ABB77875 | ABb77875 Amino aci |
| 13 | 2013 | 96.7 | 420 | 6 ABB70714 | ABb70714 Human gly |
| 14 | 2013 | 96.7 | 420 | 7 ABR44293 | ABr44293 Human gly |
| 15 | 2013 | 96.7 | 420 | 7 ADD68742 | AdD68742 Rat tau p |
| 16 | 2013 | 96.7 | 420 | 7 ADE64053 | AdE64053 Human pro |
| 17 | 2013 | 96.7 | 420 | 8 ADH09634 | AdH09634 Human hos |
| 18 | 2013 | 96.7 | 420 | 8 ADR06320 | Adr06320 Gsk-3 bet |
| 19 | 2013 | 96.7 | 420 | 8 ADR06317 | Adr06317 Gsk-3 bet |
| 20 | 2013 | 96.7 | 420 | 9 ADY64106 | AdY64106 Human gly |
| 21 | 2013 | 96.7 | 420 | 9 AEA39562 | Aea39562 Human gly |
| 22 | 2013 | 96.7 | 420 | 9 AEA39564 | Aea39564 Mouse gly |
| 23 | 2013 | 96.7 | 420 | 9 AEB28124 | Aeb28124 Human gly |
| 24 | 2013 | 96.7 | 428 | 7 ADC50594 | Adc50594 Human tau |

| | | | | | |
|----|--------|------|-----|------------|--------------------|
| 25 | 2010 | 96.6 | 420 | 2 AAR61326 | Aar61326 Tau-prote |
| 26 | 2010 | 96.6 | 420 | 6 ABR82106 | ABr82106 Human gly |
| 27 | 2010 | 96.6 | 420 | 7 ABR44289 | ABr44289 Human gly |
| 28 | 2010 | 96.6 | 420 | 7 ADE64051 | AdE64051 Rat Prote |
| 29 | 2010 | 96.6 | 420 | 8 ADI28893 | AdI28893 Mouse gly |
| 30 | 1996.5 | 95.9 | 433 | 7 ABR44295 | ABr44295 Human gly |
| 31 | 1996.5 | 95.9 | 433 | 7 ABR44298 | ABr44298 Human gly |
| 32 | 1996.5 | 95.9 | 433 | 7 ADJ69554 | AdJ69554 Human hea |
| 33 | 1996.5 | 95.9 | 433 | 8 ADH09633 | AdH09633 Human hos |
| 34 | 1996.5 | 95.9 | 433 | 8 ADO49107 | Ado49107 Human ded |
| 35 | 1996.5 | 95.9 | 433 | 8 ADU20919 | Adu20919 Human gly |
| 36 | 1996.5 | 95.9 | 433 | 8 ADU06409 | Adu06409 Novel bro |
| 37 | 1996.5 | 95.9 | 433 | 9 AEB25735 | Aeb25735 Human and |
| 38 | 1996.5 | 95.8 | 439 | 8 ADR66057 | Adr66057 Human pro |
| 39 | 1994.5 | 95.8 | 439 | 8 ADR66399 | Adr66399 Human pro |
| 40 | 1978 | 95.1 | 385 | 8 ADY85481 | AdY85481 Catalytic |
| 41 | 1883.5 | 90.5 | 361 | 5 ABB07579 | ABb07579 Human trn |
| 42 | 1877 | 90.2 | 367 | 8 ADR06334 | Adr06334 Gsk-3 bet |
| 43 | 1877 | 90.2 | 378 | 5 ABB77877 | ABb77877 Sequence |
| 44 | 1872.5 | 90.0 | 361 | 5 ABA47983 | ABa47983 Human gly |
| 45 | 1872.5 | 90.0 | 361 | 7 ADC37107 | Adc37107 Human GSK |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| ABB07578 | ABB07578 standard; protein, 394 AA. |
| XX | AC ABB07578; |
| XX | DT 08-MAY-2002 (first entry) |
| XX | DE Human truncated GSK3beta polypeptide 557. |
| XX | KW GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; neurotrophic; human; |
| KW | Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy. |
| OS | Homo sapiens. |
| XX | Key location/Qualifiers |
| XX | Peptide 1..10 "Glu-tag and Gly linker" |
| FT | 11..394 |
| FT | /note="truncated GSK3beta" |
| XX | PN MO200210357-A2. |
| XX | PD 07-FEB-2002. |
| XX | PF 25-JUL-2001; 2001WO-US023539. |
| XX | PR 27-JUL-2000; 2000US-0221242P. |
| XX | PA (CHIR) CHIRON CORP. |
| XX | PI Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EX; |
| XX | Colt DG, Nguyen SH, Medina-Selby A; |
| XX | WPI: 2002-188732/24. |
| XX | DR New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids |
| XX | PT encoding them, useful for treating diseases mediated by GSK3 activity, |
| XX | including Alzheimer's disease, type 2 diabetes and inflammation. |
| PS | Claim 8; Fig 2A-B; 36pp; English. |
| XX | The invention provides glycogen synthase kinase 3 (GSK3) polypeptides |
| CC | capable of crystallisation, including GSK3alpha and GSK3beta |
| CC | polypeptides. The GSK polypeptides can be used to identify and optimise |
| CC | GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as |
| CC | pharmaceutical agents, for treating diseases mediated by GSK3 activity, |

including Alzheimer's disease, type 2 diabetes and inflammation. The present sequence represents the amino acid sequence of a truncated GSK3beta polypeptide 557

Sequence 394 AA;

Query Match 100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 2,7e-216;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEYPMEGGMSGRPRITTSFAESCKPVQPSAFGSMKVSXDGSKVTYVATPGQGPDR 60
DB 1 MEYPMEGGMSGRPRITTSFAESCKPVQPSAFGSMKVSXDGSKVTYVATPGQGPDR 60
QY 61 POEVSYDTKYVINGSGFVVYQAKLDSGELVAIKVLDKRFKRELQIMRKLDHCNTV 120
DB 61 POEVSYDTKYVINGSGFVVYQAKLDSGELVAIKVLDKRFKRELQIMRKLDHCNTV 120
QY 121 RLRYFFYSSGSKDEVLNLVDYVPETVYVARHYSRAKQTLPIYVKLYMYQLFRSLA 180
DB 121 RLRYFFYSSGSKDEVLNLVDYVPETVYVARHYSRAKQTLPIYVKLYMYQLFRSLA 180
QY 181 YHSFGICHRDIKQNLIDPDYAVLKLDFGSAKQLVGSPNVSYICSRYYRAPELIFG 240
DB 181 YHSFGICHRDIKQNLIDPDYAVLKLDFGSAKQLVGSPNVSYICSRYYRAPELIFG 240
QY 241 ATDTSIDVWSACVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIRENNPNYTE 300
DB 241 ATDTSIDVWSACVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIRENNPNYTE 300
QY 301 FKFPQIQAHPWTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPNVKH 360
DB 301 FKFPQIQAHPWTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
DB 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394

RESULT 2
AAE05998 ID AAE05998 standard; protein; 420 AA.
XX
AC AAE05998;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human glycogen synthase kinase 3-beta #1.
XX
KM Antisense: glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;
KM insulin regulation disorder; neurological disorder; Alzheimer's disease;
KM bipolar illness; inflammation; tumour; tau protein kinase I; TPX-1;
KM human.
XX
OS Homo sapiens.
XX
PN MO200152862-A1.
XX
PD 26-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001085.
XX
PR 19-JAN-2000; 2000US-00489765.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Butler MM, McKay R, Monia BP, Wyatt JR;
XX WPI, 2001-457510/49.
XX DR N-PSDB; AAD11491.
XX
PT Novel antisense compounds, particularly antisense oligonucleotides for
PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for

diagnosing, treating neurological and insulin regulation disorders.

Example 13; Page 88-90; 106pp; English.

CC The invention relates to antisense compounds targeted to nucleic acid
CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau
CC protein kinase I (TPK-I)). The antisense compound is useful for
CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in
CC cells or tissues and for treating diseases or conditions associated with
CC the enzyme such as insulin regulation disorder, in particular diabetes
CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.
CC The antisense compound is also useful for diagnosing diseases associated
CC with the expression of glycogen synthase kinase 3-beta and for
CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour
CC formation and as a research reagent. The present sequence is human
CC glycogen synthase kinase 3-beta

Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSXDGSKVTYVATPGQGPDRPOEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSXDGSKVTYVATPGQGPDRPOEVSYDTK 60
QY 71 VINGSGFVVYQAKLDSGELVAIKVLDKRFKRELQIMRKLDHCNTVRLRYFFYSSG 130
DB 61 VINGSGFVVYQAKLDSGELVAIKVLDKRFKRELQIMRKLDHCNTVRLRYFFYSSG 120
QY 131 EKQDEVYLNVLVYPETVYVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 190
DB 121 EKQDEVYLNVLVYPETVYVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 180
QY 191 DIKQNLIDPDYAVLKLDFGSAKQLVGSPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQNLIDPDYAVLKLDFGSAKQLVGSPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIRENNPNYTEFKFPQIKAMP 310
DB 241 WSAGCVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIRENNPNYTEFKFPQIKAMP 300
QY 311 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 370
DB 301 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
ABB07577 ID ABB07577 standard; protein; 420 AA.
XX
AC ABB07577;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human glycogen synthase kinase 3beta (GSK3beta) polypeptide.
XX
KM GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human;
KM Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 216
FT Peptide /note= "phosphorylated"
FT /note= ".419"
FT Peptide /note= "specifically claimed fragment"
FT 278..419

FT Peptide /note= "specifically claimed fragment"
FT 285..384
FT /note= "specifically claimed fragment"
FT 351..384
FT Peptide /note= "specifically claimed fragment"
XX
XX WO200210357-A2.
XX
XX 07-FEB-2002.
XX
XX 25-JUL-2001; 2001WO-US023539.
XX
XX 27-JUL-2000; 2000US-0221242P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY;
XX Cost DG, Nguyen SH, Medina-Selby A;
XX
XX WPI; 2002-188732/24.
XX
XX New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids
XX encoding them, useful for treating diseases mediated by GSK3 activity,
XX including Alzheimer's disease, type 2 diabetes and inflammation.
XX
XX Claim 6; Fig 1A-B; 36pp; English.
XX
XX The invention provides glycogen synthase kinase 3 (GSK3) polypeptides
XX capable of crystallization, including GSK3alpha and GSK3beta
XX polypeptides. The GSK polypeptides can be used to identify and optimize
XX GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as
XX pharmaceutical agents, for treating diseases mediated by GSK3 activity,
XX including Alzheimer's disease, type 2 diabetes and inflammation. The
XX present sequence represents the amino acid sequence of human GSK3beta
XX polypeptide
XX
XX Sequence 420 AA;
SQ
Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRRPTTSFASBCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYYDTK 70
DB 1 MSGRRPTTSFASBCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYYDTK 60
QY 71 VINGSGFGVVVQAKLCDSGELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFGVVVQAKLCDSGELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 120
QY 131 EKKDEVYLVNLVDVVPETVYVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 190
DB 121 EKKDEVYLVNLVDVVPETVYVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 180
QY 191 DIKQNLILDPDTAVLKLCDFGSAKQLVRGEPNNYSICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKQNLILDPDTAVLKLCDFGSAKQLVRGEPNNYSICSRYYRABELIFGATDYTSSIDV 240
QY 251 MSAGCVLAELLGGPIFPDGSVDQLVEIIVKLGTPREOIREMNPNTTEFFPOIKAH 310
DB 241 MSAGCVLAELLGGPIFPDGSVDQLVEIIVKLGTPREOIREMNPNTTEFFPOIKAH 300
QY 311 WTKVPRPTPEBAIALCSRLLEYTPARLTPLACANHSFFDELARDPNYKHPRGRDTPALF 370
DB 301 WTKVPRPTPEBAIALCSRLLEYTPARLTPLACANHSFFDELARDPNYKHPRGRDTPALF 360
QY 371 NFTTOELSSNPPLATILIPPHARI 394
DB 361 NFTTOELSSNPPLATILIPPHARI 384

ID ABR44294 standard; protein; 420 AA.
XX
XX ABR44294;
AC
XX
XX 18-AUG-2003 (first entry)
DT
XX
XX Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
DE
XX
XX GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
XX vunerary; antiarteriosclerotic; GSK3beta; enzyme.
XX
XX Homo sapiens.
OS
XX
XX WO2003038037-A2.
XX
XX 08-MAY-2003.
XX
XX 23-OCT-2002; 2002WO-US033909.
XX
XX 29-OCT-2001; 2001US-0350160P.
XX
XX 13-NOV-2001; 2001US-0337905P.
XX
XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
XX Walsh K;
XX
XX WPI; 2003-482140/45.
XX
XX Modulating angiogenesis, useful for treating hyperlipidemia, comprises
XX administering an angiogenesis inhibitor/promoter, such as an
XX active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3
XX activator/inhibitor.
XX
XX Disclosure; Page 100-101; 115pp; English.
XX
XX The invention relates to inhibiting/enhancing angiogenesis. The method
XX involves administering to a subject needing the treatment, an
XX angiogenesis inhibitor/promoter, such as an active/inactive glycogen
XX synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
XX where the angiogenesis modulator is administered to inhibit/enhance
XX angiogenesis in a subject. The methods are useful for treating a
XX condition associated with increased apoptotic cell death of vascular
XX endothelial cells, where the condition is characterized by lesion of
XX blood vessel wall, such as hyperlipidemia, also in the treatment of
XX myocardial infarction and in the promotion of wound healing. The present
XX sequence represents a human GSK3beta polypeptide (Genbank Accession No.
XX S53324)
XX
XX Sequence 420 AA;
SQ
Query Match 97.3%; Score 2024; DB 7; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRRPTTSFASBCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYYDTK 70
DB 1 MSGRRPTTSFASBCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGCGDRPOEVSYYDTK 60
QY 71 VINGSGFGVVVQAKLCDSGELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFGVVVQAKLCDSGELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 120
QY 131 EKKDEVYLVNLVDVVPETVYVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 190
DB 121 EKKDEVYLVNLVDVVPETVYVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 180
QY 191 DIKQNLILDPDTAVLKLCDFGSAKQLVRGEPNNYSICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKQNLILDPDTAVLKLCDFGSAKQLVRGEPNNYSICSRYYRABELIFGATDYTSSIDV 240
QY 251 MSAGCVLAELLGGPIFPDGSVDQLVEIIVKLGTPREOIREMNPNTTEFFPOIKAH 310
DB 241 MSAGCVLAELLGGPIFPDGSVDQLVEIIVKLGTPREOIREMNPNTTEFFPOIKAH 300

OY 311 WTKVFRPTPEPAALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 370
 DB 301 WTKVFRPTPEPAALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 360
 OY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384
 RESULT 5
 ADK11467
 ID ADK11467 standard; protein; 420 AA.
 AC ADK11467;
 XX
 XX 06-MAY-2004 (first entry)
 DE Human glycogen synthase kinase 3 beta protein.
 XX
 KW cytosolic; cardiovascular; immunosuppressive; nephrotoxic;
 KW antirheumatic; antirheumatic; dermatological; antipsoriatic;
 KW antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
 KW cardiovascular disorder; autoimmune disease; glomerulonephritis;
 KW rheumatoid arthritis; dermatological disorder; psoriasis;
 KW inflammatory disorder; malaria; emphysema; alopecia.
 XX
 OS Homo sapiens.
 XX MO2003040301-A2.
 PN 15-MAY-2003.
 PD 23-OCT-2002; 2002MO-GB004780.
 PE 05-NOV-2001; 2001GB-00026506.
 PR 27-NOV-2001; 2001GB-00028384.
 PR 11-FEB-2002; 2002GB-00003185.
 XX
 XX (CYCL-) CYCLACEL LTD.
 PA
 XX Deak P, Frenz L, Glover D, Midgley C;
 PI WPI; 2003-441540/41.
 XX N-PSDB; ADK11466.
 DR
 XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,
 PT preventing and/or treating disorders, such as cancer, glomerulonephritis,
 PT rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
 XX
 XX Example 27; Page 218; 265pp; English.
 PS
 XX The invention relates to novel Drosophila species DNA sequences and their
 CC encoded proteins with their corresponding human homologues. The proteins
 CC or their encoding polynucleotides are useful in a method of prevention,
 CC treatment or diagnosis of a disease in an individual, and used to
 CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC bringing the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide
 CC and/or regulating a cell division cycle function. The diseases also

CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. This sequence represents a human homolog
 CC for one of the Drosophila proteins of the invention.
 XX
 SQ Sequence 420 AA;
 Query Match 97.3%; Score 2024; DB 7; Length 420;
 Best local similarity 100.0%; Pred. No. 4.7e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 11 MSGRPTTSFAESCKPVQGPSAFGSMKVSBDKSKYTTVATPGQGPDRPQEVSYTDTK 70
 DB 1 MSGRPTTSFAESCKPVQGPSAFGSMKVSBDKSKYTTVATPGQGPDRPQEVSYTDTK 60
 OY 71 VINGSGFVVYQAKLCSGSELVAIKKYLQDKRFKQRELOIMRKLDHCNIVRLRYFYSSG 130
 DB 61 VINGSGFVVYQAKLCSGSELVAIKKYLQDKRFKQRELOIMRKLDHCNIVRLRYFYSSG 120
 OY 131 EKKDEVYLNIVLDVVPETVYRVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSGFCHR 190
 DB 121 EKKDEVYLNIVLDVVPETVYRVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSGFCHR 180
 OY 191 DIKQNLILDPDITAVLKCDFGSAKQLVRSBPVSYICSRYYRAPBELIFGATDYSIDV 250
 DB 181 DIKQNLILDPDITAVLKCDFGSAKQLVRSBPVSYICSRYYRAPBELIFGATDYSIDV 240
 OY 251 WSAGCVIAELLIGQPIPPGDSGVQDVEIIVKLTGTPPREQIREMNPVYTEFKFPQIAHP 310
 DB 241 WSAGCVIAELLIGQPIPPGDSGVQDVEIIVKLTGTPPREQIREMNPVYTEFKFPQIAHP 300
 OY 311 WTKVFRPTPEPAALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 370
 DB 301 WTKVFRPTPEPAALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 360
 OY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384
 RESULT 6
 ADH09637
 ID ADH09637 standard; protein; 420 AA.
 XX
 AC ADH09637;
 XX
 XX 11-MAR-2004 (first entry)
 DT
 XX Human host factor protein, SEQ ID NO 165.
 DE
 XX antiviral; host factor; retrovirus; HIV; human.
 KW
 XX Homo sapiens.
 OS
 XX MO2003094847-A2.
 PN 20-NOV-2003.
 PD 07-MAY-2003; 2003MO-US014382.
 PE 07-MAY-2002; 2002US-0378711P.
 PR
 XX (UYEM-) UNIV EMORY.
 PA
 XX Devine SE;
 PI WPI; 2004-011998/01.
 XX
 DR Identifying an antiviral compound useful for treating HIV comprises
 PT exposing a cell that expresses a host factor to a candidate compound to
 PT identify an agent that inhibits the expression or activity of the host
 PT factor.

XX Claim 13; SEQ ID NO 165; 141pp; English.
PS
XX The invention relates to a novel method for identifying an antiviral
CC compound. The novel method comprises exposing a cell that expresses a
CC host factor to a candidate compound to identify an agent that inhibits
CC the expression or activity of the host factor. The novel method involves
CC identifying an antiviral compound comprising exposing a first cell that
CC expresses a host factor to a candidate compound, determining whether the
CC candidate compound inhibits the expression or activity of the host factor
CC in the first cell, where a candidate compound that inhibits the
CC expression or activity of the host factor in the first cell is a
CC potential antiviral compound, exposing a second cell to the potential
CC antiviral compound and a retrovirus, and determining whether the compound
CC inhibits the ability of the retrovirus to infect or replicate within the
CC second cell, where a potential antiviral compound that inhibits the
CC ability of the retrovirus to infect the second cell is an antiviral
CC compound. The method is useful in identifying antiviral agents, including
CC those that are effective against retroviruses, such as HIV. This sequence
CC represents a human host factor protein used in the antiviral
CC identification method of the invention.
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRRTSPAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGCGPDRPOEVSYDTK 70
DB 1 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGCGPDRPOEVSYDTK 60
QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKQDEVYINLVLDVYPPETVYVARHYSRAKQTLPIYIVKLWYQLFRSLATYHSGICHR 190
DB 121 EKQDEVYINLVLDVYPPETVYVARHYSRAKQTLPIYIVKLWYQLFRSLATYHSGICHR 180
QY 191 DIKPNLLDPTDPTAVLKLCDFGSAKQVRSGEPNVSYICSRYYRABELIFGATDYSIDV 250
DB 181 DIKPNLLDPTDPTAVLKLCDFGSAKQVRSGEPNVSYICSRYYRABELIFGATDYSIDV 240
QY 251 WSAGCVLAELLLGQPIFPDGSQVQLVEIIVKLTGPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLLGQPIFPDGSQVQLVEIIVKLTGPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVRRPRTPPPAIALCSRLLEYTPPTARLTPEACAHSPFDLDRPNVGHNGRDTPALF 370
DB 301 WTKVRRPRTPPPAIALCSRLLEYTPPTARLTPEACAHSPFDLDRPNVGHNGRDTPALF 360
QY 371 NFFTOLSSNPPLATITLIPPHARI 394
DB 361 NFFTOLSSNPPLATITLIPPHARI 384
RESULT 7
ADRA40191
ID ADRA40191 standard; protein; 420 AA.
XX
AC ADRA40191;
XX
DT 18-NOV-2004 (first entry)
DE Human glycogen synthase kinase 3 beta (GSK3beta) (1521) protein.
XX
XX haematological; cytosolic; erythroid; anaemia; erythrocytosis;
KM bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;
KM T-cells; neutropenia; gene therapy; human;
XX glycogen synthase kinase 3 beta; GSK3beta; enzyme.
OS Homo sapiens.

XX
PN WO2004072242-A2.
XX
PD 26-AUG-2004.
XX
XX 05-FEB-2004; 2004WO-US003417.
XX
XX 05-FEB-2003; 2003US-0445241P.
PR 18-FEB-2003; 2003US-0448389P.
PR 20-MAR-2003; 2003US-0456320P.
PR 03-APR-2003; 2003US-0460279P.
PR 28-APR-2003; 2003US-0465924P.
PR 13-MAY-2003; 2003US-0470052P.
PR 26-AUG-2003; 2003US-0498106P.
PR 04-SEP-2003; 2003US-0500179P.
PR 15-SEP-2003; 2003US-0502909P.
PR 10-OCT-2003; 2003US-0510351P.
PR 17-OCT-2003; 2003US-0512380P.
XX
XX (MILL-) MILLENNITUM PHARM INC.
XX
XX Kelly LM, Carroll JM, Farlow D, Healy A;
XX
XX WPI; 2004-625850/60.
XX
DR N-PESDB; ADRA40190.
XX
XX Identifying a compound capable of treating a hematological disorder
PT comprises combining a compound to be tested with a polypeptide related
PT with the disorder under conditions suitable for binding of the test
PT compound to the polypeptide.
PS
XX Claim 1; SEQ ID NO 72; 321pp; English.
XX
XX The invention relates to a novel method for identifying a compound
CC capable of treating a hematological disorder which comprises combining a
CC compound to be tested with a specific polypeptide under conditions
CC suitable for binding of the test compound to the polypeptide. The method
CC of the invention has hematological and cytosolic applications and may
CC be useful for identifying compounds for treating a hematological
CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
CC identified may be utilised during gene therapy procedures. The current
CC sequence is that of a human haematological disorder-related protein of
CC the invention.
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRRTSPAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGCGPDRPOEVSYDTK 70
DB 1 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKDSKVTTVVATPGCGPDRPOEVSYDTK 60
QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKQDEVYINLVLDVYPPETVYVARHYSRAKQTLPIYIVKLWYQLFRSLATYHSGICHR 190
DB 121 EKQDEVYINLVLDVYPPETVYVARHYSRAKQTLPIYIVKLWYQLFRSLATYHSGICHR 180
QY 191 DIKPNLLDPTDPTAVLKLCDFGSAKQVRSGEPNVSYICSRYYRABELIFGATDYSIDV 250
DB 181 DIKPNLLDPTDPTAVLKLCDFGSAKQVRSGEPNVSYICSRYYRABELIFGATDYSIDV 240
QY 251 WSAGCVLAELLLGQPIFPDGSQVQLVEIIVKLTGPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLLGQPIFPDGSQVQLVEIIVKLTGPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVRRPRTPPPAIALCSRLLEYTPPTARLTPEACAHSPFDLDRPNVGHNGRDTPALF 370

Db 301 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELBDPNNVKGHNGRDTPALF 360
Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 8
ADSS92965
ID ADSS92965 standard; protein; 420 AA.
XX
AC ADSS92965;
XX
DT 02-DEC-2004 (first entry)
XX
DE Glycogen synthase kinase 3 beta.
XX
KM cytostatic; gene therapy; human;
KM branching morphogenesis modulating agent; MBM agent.
XX
OS Homo sapiens.
XX
PN MO2004037990-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003MO-US033549.
XX
PR 23-OCT-2002; 2002US-0420554P.
PR 30-DEC-2002; 2002US-0436941P.
XX
PA (EXEL-) EXELIXIS INC.
PI Plowman GD, Karim FD, Swimmer C, Haback HA, Koblizek TI,
PI Schulte-Merker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
PI Odenthal JH, Scheel JK, Will TR, Jin Y, Bjerke LM, Hal B,
PI Adamkiewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
PI Nicoll M;
XX
XX WPI: 2004-365506/34.
DR N-PSDB; ADS92934.
XX
XX Identifying a candidate branching morphogenesis modulating agent for
PT treating cancer comprises contacting the assay system comprising a MBM
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
XX Example 3; SEQ ID NO 36; 179pp; English.

CC The invention describes a method of identifying a candidate branching
CC morphogenesis modulating (MBM) agent. The method comprises: providing an
CC assay system comprising a MBM polypeptide or nucleic acid; contacting the
CC assay system with a test agent under conditions where the system provides
CC a reference activity, except for the presence of the test agent; and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate branching morphogenesis
CC modulating agent. Also described are: a method of modulating branching
CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
CC in a patient. The method is useful in identifying a candidate branching
CC morphogenesis modulating agent for preparing a composition for diagnosing
CC or treating cancer. This is the amino acid sequence of a human branching
CC morphogenesis modulating (MBM) protein.
XX
SQ Sequence 420 AA;

Query March 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. NO. 4.7e-210; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0;

Qy 11 MSGRPRTTSFAESCCKPVQQPSAFGSMKVSRLKDSKVTTVATPQGGPDRPQEVSYDTTK 70
|||||

Db 1 MSGRPRTTSFAESCCKPVQQPSAFGSMKVSRLKDSKVTTVATPQGGPDRPQEVSYDTTK 60
Qy 71 VINGSGFVYVQAALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHGNIVRLRYFPYSSG 130
Db 61 VINGSGFVYVQAALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHGNIVRLRYFPYSSG 120
Qy 131 EKDQEVNLNLVDVPEVTVRVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDQEVNLNLVDVPEVTVRVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFGICHR 180
Qy 191 DIKPQNLILDPDTRAVLKLCDPGSAKKQLVRGSPNVSYICSRYYRABELIFGATDYSIDV 250
Db 181 DIKPQNLILDPDTRAVLKLCDPGSAKKQLVRGSPNVSYICSRYYRABELIFGATDYSIDV 240
Qy 251 MSAGCVLAELLGGPIRPGSGVDQVLEIIKVLTGTPREQIREKNPNYTEKFPQIKAMP 310
Db 241 MSAGCVLAELLGGPIRPGSGVDQVLEIIKVLTGTPREQIREKNPNYTEKFPQIKAMP 300
Qy 311 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELBDPNNVKGHNGRDTPALF 370
Db 301 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELBDPNNVKGHNGRDTPALF 360
Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 9
ADT92555
ID ADT92555 standard; protein; 420 AA.
XX
AC ADT92555;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human glycogen synthase kinase-3-related protein - SEQ ID 1.
XX
KM neurodegenerative drug; glycogen synthase kinase-3; GSK-3;
KM neurological disease; Parkinson's disease; Alzheimer's disease;
KM Down's syndrome; cerebrovascular accident; stroke; spinal injury;
KM Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;
KM epilepsy; anxiety disorder; schizophrenia; depression;
KM manic-depressive psychosis.
XX
XX Homo sapiens.
XX
XX MO2004091663-A1.
XX
XX 28-OCT-2004.
XX
XX 16-APR-2004; 2004MO-JP005503.
XX
XX 18-APR-2003; 2003JP-00114579.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Morishita T, Sakurada K, Suzuki K, Ikeda S;
XX
DR WPI: 2004-784511/77.
DR N-PSDB; ADT92556.
XX
XX Neurodegenerative drug for treating neurological disease e.g. Parkinson's
PT disease, Alzheimer's disease and Down's syndrome, contains substance
PT which inhibits activity of glycogen synthase kinase-3 as active
PT ingredient.
XX
XX Disclosure; SEQ ID NO 1; 115pp; Japanese.
XX
XX The invention comprises a neurodegenerative drug that inhibits the
CC activity of glycogen synthase kinase-3 (GSK-3). The neurodegenerative
CC drug of the invention is useful for treating neurological disease, such
CC as: Parkinson's disease, Alzheimer's disease, Down's syndrome,
CC cerebrovascular accident, stroke, spinal injury, Huntington's chorea,

multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety disorder, schizophrenia, depression and manic-depressive psychosis. The present human protein is used in the exemplification of the invention.

Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;

Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 11 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGRDREVS YTDTK 70
DB 1 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGRDREVS YTDTK 60
QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLODKRFKRELIQMRKLDHCNIVRLRFFYS SG 130
DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLODKRFKRELIQMRKLDHCNIVRLRFFYS SG 120
QY 131 EKKDEVYNTLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYTHSFGICHR 190
DB 121 EKKDEVYNTLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYTHSFGICHR 180
QY 191 DIKPNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKPNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPPEALALCSRLLEYTPARLTPLCAHSPFDLDRPNVKGHRDTPALF 370
DB 301 WTKVFRPRTPPEALALCSRLLEYTPARLTPLCAHSPFDLDRPNVKGHRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
```

RESULT 10
ADRO6333
ID ADRO6333 standard; protein; 414 AA.

AC ADRO6333;

DT 07-OCT-2004 (first entry)

DE p38-alpha kinase, SEQ ID 31.

XX Switch control ligand; switch control pocket;

KW protein activity modulation; human; p38-alpha kinase; enzyme.

XX Homo sapiens.

PN WO2004061084-A2.

PD 22-JUL-2004.

PF 26-DEC-2003; 2003WO-US041450.

PR 31-DEC-2002; 2002US-0437304P.

PR 31-DEC-2002; 2002US-0437403P.

PR 31-DEC-2002; 2002US-0437415P.

PR 18-APR-2003; 2003US-0463804P.

PR 24-DEC-2003; 53US-00463804.

PA (DECI-) DECIPHERA PHARM INC.

PI Flynn DL, Petrillo PA;

DR WPI; 2004-534376/51.

PT Identifying molecules that interact with specific naturally occurring
PT proteins for modulating protein activity, comprises identifying molecules
PT that bind with the protein at the region of the pocket to regulate
PT activity of the protein.

XX Disclosure; SEQ ID NO 31; 204pp; English.

CC The present invention relates to a method for identifying molecules,
CC which interact with proteins e.g. enzymes, receptors, or signaling
CC proteins, in order to regulate the activity of the proteins. The method
CC comprises: identifying a switch control ligand forming a part of the
CC protein; identifying a switch control pocket forming a part of the
CC protein and which interacts with the switch control ligand, where the
CC ligand interacting in vivo with the pocket to regulate the conformation
CC and biological activity of the protein so that the protein will assume a
CC first conformation and a first biological activity upon the ligand-pocket
CC interaction, and will assume a second, different conformation and a
CC biological activity in the absence of the ligand-pocket interaction;
CC providing respective samples of the protein in the first and second
CC conformations; and screening at least one of the samples against one or
CC more candidate molecules by contacting the molecules and one sample, and
CC identifying small molecules which bind with the protein at the region of
CC the pocket in order to regulate the activity of the protein. The method
CC is useful for modulating protein activity and for the identification of
CC new pharmacological compounds and for treatment modalities. The present
CC sequence is p38-alpha kinase for which a switch control ligand was
CC produced.

XX Sequence 414 AA;

Query Match 96.7%; Score 2013; DB 8; Length 414;

Best Local Similarity 99.7%; Pred. No. 7.2e-209; Indels 0; Gaps 0;

Matches 383; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
QY 11 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGRDREVS YTDTK 70
DB 1 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGRDREVS YTDTK 60
QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLODKRFKRELIQMRKLDHCNIVRLRFFYS SG 130
DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLODKRFKRELIQMRKLDHCNIVRLRFFYS SG 120
QY 131 EKKDEVYNTLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYTHSFGICHR 190
DB 121 EKKDEVYNTLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYTHSFGICHR 180
QY 191 DIKPNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKPNLLDPTAVLKLCDGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPPEALALCSRLLEYTPARLTPLCAHSPFDLDRPNVKGHRDTPALF 370
DB 301 WTKVFRPRTPPEALALCSRLLEYTPARLTPLCAHSPFDLDRPNVKGHRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
```

RESULT 11
AAR61327
ID AAR61327 standard; protein; 420 AA.

AC AAR61327;

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX Tau-protein kinase I (TPK-I), Alzheimer's disease.

XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease.
 KM Ractus ractus.
 OS EP616032-A2.
 XX 21-SEP-1994.
 PD 01-MAR-1994; 94EP-00103057.
 XX 02-MAR-1993; 93JP-00041160.
 PR 22-MAR-1993; 93JP-00085143.
 PR 02-AUG-1993; 93JP-00191246.
 XX (MITU) MITSUBISHI KASEI CORP.
 PA (MITU) MITSUBISHI CHEM CORP.
 XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A,
 PI Sato S;
 XX WPI; 1994-287181/36.
 DR N-PSDB; AA067459.
 XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-
 PT protein providing means for prevention and treatment of Alzheimer's
 PT disease.
 XX Claim 4; Page 18; 30pp; English.
 XX AA067459 codes for a newly isolated tau-protein kinase I enzyme (TPK-I),
 CC shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a
 CC rat fetus brain cDNA library, and was expressed in insect cells. TPK-I
 CC acts specifically on tau-protein, which is thought to be involved in
 CC Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped
 CC that the characterization of TPK-I may lead to development of new agents
 CC for the prevention and therapy of these diseases. (Updated on 25-MAR-2003
 CC to correct pw field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 420 AA;
 SQ
 Query Match 96.7%; Score 2013; DB 2; Length 420;
 Best Local Similarity 99.7%; Pred. No. 7.4e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVS RDKSGSKVTTVVATPGQGPDRPQEVSYTDTK 70
 DB 1 MSGRPRTTSPAESCKPVQPSAFSGSMKVS RDKSGSKVTTVVATPGQGPDRPQEVSYTDTK 60
 QY 71 VINGSGFGVYQAKLDCDSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 130
 DB 61 VINGSGFGVYQAKLDCDSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 120
 QY 131 EKDDEVYLVNLVDYVPEYTVRVARHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGFICHR 190
 DB 121 EKDDEVYLVNLVDYVPEYTVRVARHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGFICHR 180
 QY 191 DIKPQNLDPDPTAVLKLCDGSAKQLVGEPNVSYICSRYYRABELIFGATDYSIDV 250
 DB 181 DIKPQNLDPDPTAVLKLCDGSAKQLVGEPNVSYICSRYYRABELIFGATDYSIDV 240
 QY 251 WSAGCVLAELLGQPIFFGDSGVOLVETIIVLGTPTREQIREMNPNTTEKFFQIKRHP 310
 DB 241 WSAGCVLAELLGQPIFFGDSGVOLVETIIVLGTPTREQIREMNPNTTEKFFQIKRHP 300
 QY 311 WTKKFRPTPEALATLSRILEYTPARLTPLBACASFDELKDOPNKHNGRDTPLAF 370
 DB 301 WTKKFRPTPEALATLSRILEYTPARLTPLBACASFDELKDOPNKHNGRDTPLAF 360
 QY 371 NFFTQELSSNPPLATILIPPHARI 394
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 12
 AB877875
 ID AB877875 standard; peptide; 420 AA.
 XX
 AC AB877875;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Amino acid sequence of glycogen synthase kinase 3 isoform beta.
 XX
 XX Glycogen synthase kinase 3 beta; GSK3beta; T-cell lymphoma; stroke;
 KM Type II diabetes mellitus; obesity; neurodegenerative disorder; cancer;
 KM Alzheimer's disease; mood disorder; depression; schizophrenia;
 KM cyclin-dependent kinase 2; substrate; protein coordinate data.
 XX
 OS Homo sapiens.
 XX WO200250254-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 18-DEC-2001; 2001WO-GB005632.
 XX
 XX 18-DEC-2000; 2000GB-00030846.
 PR 14-AUG-2001; 2001GB-00019796.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 PI Bax B, Brown M, Relch A;
 XX
 XX WPI; 2002-519885/55.
 DR
 XX Novel crystal structures comprising glycogen synthase kinase (GSK)-3 beta
 PT protein or crystal structure comprising a GSK-3 beta: frequently
 PT rearranged in advanced T-cell lymphomas (PRAT)-tide complex in
 PT crystalline form.
 XX
 XX Claim 6; Page 23; 327pp; English.
 PS
 XX The specification describes the structure of glycogen synthase kinase
 CC (GSK)3beta protein in crystalline form. GSK3beta is frequently rearranged
 CC in advanced T-cell lymphomas. The crystalline structure of GSK3beta is
 CC useful in the design or selection of potential inhibitors and/or
 CC activators of GSK3beta kinase activity. Such inhibitors and activators
 CC are useful for treating Type II diabetes mellitus, obesity,
 CC neurodegenerative disorders such as Alzheimer's disease, stroke and mood
 CC disorders such as bipolar and unipolar depression, schizophrenia, cancer,
 CC in humans. Because GSK3beta may crystallize in more than one crystal
 CC form, the structure coordinates of GSK3 or its portions are particularly
 CC useful to solve the structure of other crystal forms of GSK3. They may
 CC also be used to solve the structure of GSK3 mutants, GSK3 co-complexes,
 CC or of the crystalline form of any other protein, particularly kinases
 CC with significant amino acid sequence homology to any functional domain of
 CC GSK3. The present sequence represents the beta isoform of GSK3, GSK3beta
 XX
 SQ Sequence 420 AA;
 Query Match 96.7%; Score 2013; DB 5; Length 420;
 Best Local Similarity 99.7%; Pred. No. 7.4e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVS RDKSGSKVTTVVATPGQGPDRPQEVSYTDTK 70
 DB 1 MSGRPRTTSPAESCKPVQPSAFSGSMKVS RDKSGSKVTTVVATPGQGPDRPQEVSYTDTK 60
 QY 71 VINGSGFGVYQAKLDCDSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 130
 DB 61 VINGSGFGVYQAKLDCDSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 120
 QY 131 EKDDEVYLVNLVDYVPEYTVRVARHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGFICHR 190
 DB 121 EKDDEVYLVNLVDYVPEYTVRVARHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGFICHR 180

QY 191 DIKPNLLDPDTAVLKLCDPGSAKOLVRGEPNVSICSRYYRAPELIFGATDYSIDV 250
 DB 181 DIKPNLLDPDTAVLKLCDPGSAKOLVRGEPNVSICSRYYRAPELIFGATDYSIDV 240
 QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTEQIREMNPNTTEKFPQIKAH 310
 DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTEQIREMNPNTTEKFPQIKAH 300
 QY 311 WTKVFRPPTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELRDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPPTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELRDPNVKHPNGRDTPALF 360
 QY 371 NPTTOELSSNPPLATILIPPHARI 394
 DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 13
 ABR70714
 ID ABR70714 standard; protein; 420 AA.
 AC ABR70714;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Human glycogen synthase kinase-3 beta.
 XX
 KW Human; enzyme; glycogen synthase kinase-3 beta; protein co-ordinate data;
 KW noctropic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;
 KW antiinflammatory; cardiovascular; antiallergic; antiaesthetic; GSK-3;
 KW antiparkinsonian; anticonvulsant; dermatological; vasotropic; GSK-3;
 KW schizophrechia; Alzheimer's disease; diabetes; autoimmune disease;
 KW inflammatory disease; metabolic; neurological; neurodegenerative;
 KW cardiovascular disease; allergy; asthma; Huntington's disease;
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;
 KW amyotrophic lateral sclerosis; multiple sclerosis; kinase;
 KW cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO200288078-A2.
 XX
 PD 07-NOV-2002.
 XX
 PE 29-APR-2002; 2002WO-US013511.
 XX
 PR 30-APR-2001; 2001US-0287366P.
 PR 08-JUN-2001; 2001US-0297094P.
 PR 27-FEB-2002; 2002US-0361899P.
 PA (VERT-) VERTEX PHARM INC.
 XX
 PI Ter Haar E, Swenson L, Green J, Arnott MJ;
 DR WPI; 2003-247844/24.
 XX
 PT New pyrazolo(3,4-c)pyridazine derivatives are glucogen synthase kinase -3
 PT inhibitor useful for treating e.g. schizoprenia, Alzheimer's disease,
 PT diabetes, autoimmune diseases, allergy, asthma, multiple sclerosis, and
 PT baldness.
 XX
 XX Claim 36; Page 777-778; 778bp; English.
 XX
 CC The present invention relates to novel pyrazolo(3,4-c)pyridazine
 CC derivatives, which have glucogen synthase kinase-3 (GSK-3) inhibitory
 CC activity. The derivatives are useful for inhibiting beta-catenin
 CC phosphorylation and hyperphosphorylated Tau protein production in a
 CC patient and GSK-3 activity in a patient or in a biological sample. The
 CC derivatives are also useful for treating schizoprenia, Alzheimer's
 CC disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,
 CC neurological and neurodegenerative diseases, cardiovascular diseases,
 CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related

CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.
 CC The present sequence is human GSK-3 beta, used to illustrate the
 CC invention. GSK-3 beta is a serine/threonine protein kinase
 XX
 SQ Sequence 420 AA;
 Query Match 96.7%; Score 2013; DB 6; Length 420;
 Best Local Similarity 99.7%; Pred. No. 7,4e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSFASCKPVOQPSAFSGMKYSRDKDSKVTTVATPQGGDRQEVSYTDTK 70
 DB 1 MSGRPRTTSFASCKPVOQPSAFSGMKYSRDKDSKVTTVATPQGGDRQEVSYTDTK 60
 QY 71 VINGSGFCVVYQAKLCSGSELVAIKVLDKRRFNKRELQIKRLDHCNIVLRFFYSYG 130
 DB 61 VINGSGFCVVYQAKLCSGSELVAIKVLDKRRFNKRELQIKRLDHCNIVLRFFYSYG 120
 QY 131 EKKQEVYINLVLDVPEVTVVVAHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKKQEVYINLVLDVPEVTVVVAHYSRAKQTLPIYIVKLYMYQLFRSLAYIHSGICHR 180
 QY 191 DIKPNLLDPDTAVLKLCDPGSAKOLVRGEPNVSICSRYYRAPELIFGATDYSIDV 250
 DB 181 DIKPNLLDPDTAVLKLCDPGSAKOLVRGEPNVSICSRYYRAPELIFGATDYSIDV 240
 QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTEQIREMNPNTTEKFPQIKAH 310
 DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTEQIREMNPNTTEKFPQIKAH 300
 QY 311 WTKVFRPPTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELRDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPPTPEPAIALCSRLLEYTPPTARLTPLACAHSPFDELRDPNVKHPNGRDTPALF 360
 QY 371 NPTTOELSSNPPLATILIPPHARI 394
 DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 14
 ABR44293
 ID ABR44293 standard; protein; 420 AA.
 AC ABR44293;
 XX
 DT 18-AUG-2003 (first entry)
 XX
 DE Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
 XX
 KW GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
 KW vulnery; antiarteriosclerotic; GSK3beta; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003038037-A2.
 XX
 PD 08-MAY-2003.
 XX
 PE 23-OCT-2002; 2002WO-US033909.
 XX
 PR 29-OCT-2001; 2001US-0350160P.
 PR 13-NOV-2001; 2001US-0337905P.
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
 XX
 PI Walsh K;
 DR WPI; 2003-482140/45.
 XX
 PT Modulating angiogenesis, useful for treating hyperlipidemia, comprises
 PT administering an angiogenesis inhibitor/promoter, such as an
 PT active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3

PT activator/inhibitor.
XX
PS Disclosure; Page 97-99; 115pp; English.
XX
CC The invention relates to inhibiting/enhancing angiogenesis. The method
XX involves administering to a subject needing the treatment, an
CC angiogenesis inhibitor/promoter, such as an active/inactive glycogen
CC synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
CC where the angiogenesis modulator is administered to inhibit/enhance
CC angiogenesis in a subject. The methods are useful for treating a
CC condition associated with increased apoptotic cell death of vascular
CC endothelial cells, where the condition is characterized by lesion of
CC blood vessel wall, such as hyperlipidemia, also in the treatment of
CC myocardial infarction and in the promotion of wound healing. The present
CC sequence represents a human GSK3beta polypeptide (Genbank Accession No.
CC P49841)
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.4e-209; Indels 0; Gaps 0;
Matches 383; Conservative 0; Mismatches 1;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFGVVYQAKLCDSGELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSYG 130
DB 61 VINGSGFGVVYQAKLCDSGELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSGICHR 190
DB 121 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSGICHR 180
QY 191 DIRQNLILDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIRQNLILDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRREQIREMNPVTEFKFPQIKAH 310
DB 241 WSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRREQIREMNPVTEFKFPQIKAH 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 15
ADD68742
ID ADD68742 standard; protein; 420 AA.
XX
AC ADD68742;
XX
DT 15-JAN-2004 (first entry)
XX
DE Rat tau phosphorylation-related protein.
XX
KW tau; phosphoenzyme I; Alzheimer's disease; senile dementia;
KW serine-threonine phosphorylation; rat.
XX
OS Rattus sp.
XX
PN JP2002335983-A.
XX
PD 26-NOV-2002.
XX
PF 03-JUL-1992; 2002JP-00129146.
XX

PR 03-JUL-1992; 92JP-00177241.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 2003-460769/44.
XX
XX N-PSDB; ADD68695.
PT Phosphorylation of tau protein.
PS Disclosure; Page 11-13; 29pp; Japanese.
XX
CC The invention relates to a novel method for the phosphorylation of tau
CC protein in which tau protein or its partial peptide is phosphorylated by
CC the action of phosphoenzyme I, a serine-threonine phospholase. The
CC method of the invention may be used for elucidation of the cause of
CC Alzheimer's disease and Alzheimer type senile dementia. The current
CC sequence is that of the rat tau phosphorylation-related protein of the
CC invention.
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.4e-209; Indels 0; Gaps 0;
Matches 383; Conservative 0; Mismatches 1;

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DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFGVVYQAKLCDSGELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSYG 130
DB 61 VINGSGFGVVYQAKLCDSGELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSGICHR 190
DB 121 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSGICHR 180
QY 191 DIRQNLILDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIRQNLILDPDTAVLKLCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRREQIREMNPVTEFKFPQIKAH 310
DB 241 WSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRREQIREMNPVTEFKFPQIKAH 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLEACAHSPFDELDPNVKHPNGRDPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

Search completed: May 16, 2006, 15:05:37
Job time : 187 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2006, 15:20:57 ; Search time 167 Seconds
(without alignments)
985.777 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081
Sequence: 1 MEYPMMEGSGSGRPRTTSF.....OELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1667569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 2081 | 100.0 | 394 | 3 | US-09-916-109-2 |
| 2 | 2081 | 100.0 | 394 | 4 | US-10-211-412A-2 |
| 3 | 2081 | 100.0 | 394 | 4 | US-10-689-461-2 |
| 4 | 2024 | 97.3 | 420 | 3 | US-09-916-109-1 |
| 5 | 2024 | 97.3 | 420 | 4 | US-10-211-412A-1 |
| 6 | 2024 | 97.3 | 420 | 4 | US-10-278-759-7 |
| 7 | 2024 | 97.3 | 420 | 5 | US-10-482-525-4 |
| 8 | 2024 | 97.3 | 420 | 5 | US-10-772-632-72 |
| 9 | 2024 | 97.3 | 420 | 5 | US-10-689-461-1 |
| 10 | 2024 | 97.3 | 420 | 5 | US-10-840-060-257 |
| 11 | 2013 | 96.7 | 414 | 4 | US-10-746-545-31 |
| 12 | 2013 | 96.7 | 420 | 4 | US-10-278-759-6 |
| 13 | 2013 | 96.7 | 420 | 4 | US-10-135-255-1 |
| 14 | 2013 | 96.7 | 420 | 4 | US-10-746-545-15 |
| 15 | 2013 | 96.7 | 420 | 4 | US-10-746-545-18 |
| 16 | 2010 | 96.6 | 420 | 4 | US-10-278-759-2 |
| 17 | 2010 | 96.6 | 420 | 4 | US-10-322-153A-1 |
| 18 | 2010 | 96.6 | 420 | 4 | US-10-613-728-8 |
| 19 | 1997 | 96.0 | 385 | 4 | US-10-664-421-53 |
| 20 | 1997 | 96.0 | 385 | 5 | US-10-941-625-53 |
| 21 | 1996.5 | 95.9 | 433 | 4 | US-10-278-759-8 |
| 22 | 1996.5 | 95.9 | 433 | 4 | US-10-278-759-14 |
| 23 | 1996.5 | 95.9 | 433 | 4 | US-10-302-812-62 |
| 24 | 1996.5 | 95.9 | 433 | 4 | US-10-408-765A-1360 |
| 25 | 1996.5 | 90.5 | 433 | 5 | US-10-828-669-5 |
| 26 | 1883.5 | 90.5 | 361 | 3 | US-09-916-109-3 |
| 27 | 1883.5 | 90.5 | 361 | 4 | US-10-211-412A-3 |

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| 28 | 1883.5 | 90.5 | 361 | 5 | US-10-689-461-3 | Sequence 3, Appl1 |
| 29 | 1877 | 90.2 | 367 | 4 | US-10-746-545-32 | Sequence 32, Appl1 |
| 30 | 1872.5 | 90.0 | 361 | 4 | US-10-450-422-1 | Sequence 1, Appl1 |
| 31 | 1817 | 87.3 | 352 | 4 | US-10-664-421-31 | Sequence 11, Appl1 |
| 32 | 1817 | 87.3 | 352 | 4 | US-10-746-545-16 | Sequence 16, Appl1 |
| 33 | 1817 | 87.3 | 352 | 4 | US-10-746-545-17 | Sequence 17, Appl1 |
| 34 | 1817 | 87.3 | 352 | 5 | US-10-941-635-11 | Sequence 31, Appl1 |
| 35 | 1817 | 87.3 | 352 | 6 | US-11-021-951-167 | Sequence 167, App |
| 36 | 1803 | 86.6 | 350 | 4 | US-10-746-545-27 | Sequence 27, Appl1 |
| 37 | 1666.5 | 80.1 | 407 | 5 | US-10-732-923-1457 | Sequence 1457, Ap |
| 38 | 1634.5 | 78.5 | 428 | 5 | US-10-491-467-13 | Sequence 13, Appl1 |
| 39 | 1609 | 77.3 | 447 | 3 | US-09-916-109-5 | Sequence 5, Appl1 |
| 40 | 1609 | 77.3 | 447 | 4 | US-10-211-412A-5 | Sequence 5, Appl1 |
| 41 | 1609 | 77.3 | 447 | 5 | US-10-689-461-5 | Sequence 5, Appl1 |
| 42 | 1609 | 77.3 | 483 | 3 | US-09-916-109-4 | Sequence 4, Appl1 |
| 43 | 1609 | 77.3 | 483 | 4 | US-10-211-412A-4 | Sequence 4, Appl1 |
| 44 | 1609 | 77.3 | 483 | 4 | US-10-278-759-3 | Sequence 3, Appl1 |
| 45 | 1609 | 77.3 | 483 | 4 | US-10-278-759-4 | Sequence 4, Appl1 |

ALIGNMENTS

| | | | | | | | | | |
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| RESULT 1 | | | | | | | | | |
| US-09-916-109-2 | | | | | | | | | |
| Sequence 2, Application US/09916109 | | | | | | | | | |
| Patent No. US20020082408A1 | | | | | | | | | |
| GENERAL INFORMATION: | | | | | | | | | |
| APPLICANT: Harrison, Stephen D. | | | | | | | | | |
| APPLICANT: Hall, John A. | | | | | | | | | |
| APPLICANT: Calderon-Cacia, Maria | | | | | | | | | |
| APPLICANT: Zhong, Ziyang | | | | | | | | | |
| APPLICANT: Fang, Eric Y. | | | | | | | | | |
| APPLICANT: Colt, Doris G. | | | | | | | | | |
| APPLICANT: Nguyen, Steve H. | | | | | | | | | |
| APPLICANT: Medina-Selby, Angelica | | | | | | | | | |
| TITLE OF INVENTION: GSK3 POLYPEPTIDES | | | | | | | | | |
| FILE REFERENCE: PP-15876.002/200130.524 | | | | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/916.109 | | | | | | | | | |
| CURRENT FILING DATE: 2001-07-25 | | | | | | | | | |
| NUMBER OF SEQ ID NOS: 11 | | | | | | | | | |
| SOFTWARE: FastSeq for Windows Version 4.0 | | | | | | | | | |
| SEQ ID NO 2 | | | | | | | | | |
| LENGTH: 394 | | | | | | | | | |
| TYPE: PRT | | | | | | | | | |
| ORGANISM: Homo sapiens | | | | | | | | | |
| US-09-916-109-2 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Score 2081; DB 3; Length 394; | | | | | | | | | |
| Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | MEYPMMEGSGSGRPRTTSFASCSKPVQQAFAFGSMKVRDQSGKTTVVATPGQFDR | 60 | | | | | | |
| DB | 1 | MEYPMMEGSGSGRPRTTSFASCSKPVQQAFAFGSMKVRDQSGKTTVVATPGQFDR | 60 | | | | | | |
| QY | 61 | POEVSYTDTKYIGNGSEGVVQAQKCDGSELVAIKVYLDQRRFKNRELQWRKLDHCNIV | 120 | | | | | | |
| DB | 61 | POEVSYTDTKYIGNGSEGVVQAQKCDGSELVAIKVYLDQRRFKNRELQWRKLDHCNIV | 120 | | | | | | |
| QY | 121 | RLRFFPSSGSKQBEVYINLVLDVYPERVYVAHYSKAKOTLPITYIKLVMYQLEFSLA | 180 | | | | | | |
| DB | 121 | RLRFFPSSGSKQBEVYINLVLDVYPERVYVAHYSKAKOTLPITYIKLVMYQLEFSLA | 180 | | | | | | |
| QY | 181 | YIHSFGICHRDIKPNLLDPTAVLKLCDGSAKQVGRGPNVSYICSRYYRAPELIFG | 240 | | | | | | |
| DB | 181 | YIHSFGICHRDIKPNLLDPTAVLKLCDGSAKQVGRGPNVSYICSRYYRAPELIFG | 240 | | | | | | |
| QY | 241 | ATDYSYIDVWSAGCVLAELLGGPIFGDSGVQDLVEIIVKLGTPTRQIREMNPYTE | 300 | | | | | | |
| DB | 241 | ATDYSYIDVWSAGCVLAELLGGPIFGDSGVQDLVEIIVKLGTPTRQIREMNPYTE | 300 | | | | | | |
| QY | 301 | KFPOIKAHPTKVPFRPTPEALALCSRLLETPYTAULTFLBACNHSFPDELDPNVKH | 360 | | | | | | |


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Db      301 FKFPQIAHPWTQVFRPTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
Qy      361 PNGRDTPALFNFPTQELSSNPPLATILIPPHARI 394
Db      361 PNGRDTPALFNFPTQELSSNPPLATILIPPHARI 394
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RESULT 2

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US-10-211-412A-2
; Sequence 2, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/200130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-2
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Query Match      100.0%; Score 2081; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.3e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MEYPMEGGMSGRPRTTSFAESCKPVQPSAFSGMKVSRDKDGSKVTTVATPGGQDR 60
Qy      61 POEVSYDTKVIKNGSGFVYVYQAKLCDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
Db      61 POEVSYDTKVIKNGSGFVYVYQAKLCDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
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Db      121 RLRFYFSSGKDEYVNLVLDYVPEVTVRVARHYSRAKQTLPIYVYKLYMQLFRSLA 180
Qy      181 YIHSFGICHRDIPQNLILDPDPAVLKLCDFGSAKQLVREPNVSYICSRYYRAPELIIFG 240
Db      181 YIHSFGICHRDIPQNLILDPDPAVLKLCDFGSAKQLVREPNVSYICSRYYRAPELIIFG 240
Qy      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQIRENNPYTE 300
Db      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQIRENNPYTE 300
Qy      301 FKFPQIAHPWTQVFRPTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
Db      301 FKFPQIAHPWTQVFRPTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
Qy      361 PNGRDTPALFNFPTQELSSNPPLATILIPPHARI 394
Db      361 PNGRDTPALFNFPTQELSSNPPLATILIPPHARI 394
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RESULT 3

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US-10-689-461-2
; Sequence 2, Application US/10689461
; Publication No. US2005004851A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
```

```
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/689,461
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-461-2
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Query Match      100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.3e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEYPMEGGMSGRPRTTSFAESCKPVQPSAFSGMKVSRDKDGSKVTTVATPGGQDR 60
Db      1 MEYPMEGGMSGRPRTTSFAESCKPVQPSAFSGMKVSRDKDGSKVTTVATPGGQDR 60
Qy      61 POEVSYDTKVIKNGSGFVYVYQAKLCDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
Db      61 POEVSYDTKVIKNGSGFVYVYQAKLCDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
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Db      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQIRENNPYTE 300
Qy      301 FKFPQIAHPWTQVFRPTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
Db      301 FKFPQIAHPWTQVFRPTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
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Db      361 PNGRDTPALFNFPTQELSSNPPLATILIPPHARI 394
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RESULT 4

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US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. US20020082408A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-1

Query Match 97.3%; Score 2024; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 240
QY 251 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412A-1
Sequence 1, Application US/10211412A
Publication No. US20030077798A1
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876, 004/200130, 524D1
CURRENT APPLICATION NUMBER: US/10/211, 412A
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-412A-1

Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 240
QY 251 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 6
US-10-278-759-7
Sequence 7, Application US/10278759
Publication No. US20030114382A1
GENERAL INFORMATION:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
FILE REFERENCE: S01237, 70020, US
CURRENT APPLICATION NUMBER: US/10/278, 759
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: US 60/350160
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/337905
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-278-759-7

Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGDPRQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKKDEVYLVLDVYVETVYVAVAHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 250
DB 181 DIKQNLILDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYTSSIDV 240
QY 251 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEEALALCSRLLEYTPARLTPLCAHSAFFDELDPNVKHPNGRDTPALF 360

Db 301 WTKVFRPRTPEAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 7

US-10-482-524-4
; Sequence 4, Application US/10482524
; Publication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham PLC
; APPLICANT: Holder, Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4458
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB 0115570.4
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: GB 0205604.2
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-524-4

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQOPSAGSMKVSBDKSGSKYTTVATPGQDPDRPOEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQOPSAGSMKVSBDKSGSKYTTVATPGQDPDRPOEVSYTDTK 60
Qy 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIIVRLRYFFYSSG 120
Qy 131 EKDEYVNLVLDVPEPTVVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVNLVLDVPEPTVVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSFGICHR 180
Qy 191 DIKPQNLDPDPTAVLKLCDFGSAKQLVKGEPNVSYICSRYYRABELIFGATDYTSSIDV 250
Db 181 DIKPQNLDPDPTAVLKLCDFGSAKQLVKGEPNVSYICSRYYRABELIFGATDYTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTREQIREMNPVTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTREQIREMNPVTEKFPQIKAMP 300
Qy 311 WTKVFRPRTPEAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 8

US-10-772-636-72
; Sequence 72, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21944, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MPI03-01SP1RMONIM
; CURRENT APPLICATION NUMBER: US/10/772,636
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-636-72

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQOPSAGSMKVSBDKSGSKYTTVATPGQDPDRPOEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQOPSAGSMKVSBDKSGSKYTTVATPGQDPDRPOEVSYTDTK 60
Qy 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIIVRLRYFFYSSG 120
Qy 131 EKDEYVNLVLDVPEPTVVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVNLVLDVPEPTVVRVARHYSRAKQTLPIVIYVKLYMQLFRSLAYIHSFGICHR 180
Qy 191 DIKPQNLDPDPTAVLKLCDFGSAKQLVKGEPNVSYICSRYYRABELIFGATDYTSSIDV 250
Db 181 DIKPQNLDPDPTAVLKLCDFGSAKQLVKGEPNVSYICSRYYRABELIFGATDYTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTREQIREMNPVTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTREQIREMNPVTEKFPQIKAMP 300
Qy 311 WTKVFRPRTPEAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 9

US-10-689-461-1

Sequence 1, Application US/10689461
Publication No. US20050046511A1
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacela, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/JP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/689,461
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US/10/211,412
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916,109
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-689-461-1

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2,6e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKDGSKTTVVATPGQGPDRQEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKDGSKTTVVATPGQGPDRQEVSYDTK 60
QY 71 VIGNGSGVYVQAALCDSGELVAIKVLODKRFKRELOIRKIDHCNIIVLRFFYS5G 130
DB 61 VIGNGSGVYVQAALCDSGELVAIKVLODKRFKRELOIRKIDHCNIIVLRFFYS5G 120
QY 131 EKQDEVYLVNLDVVPETVVRVARRHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKQDEVYLVNLDVVPETVVRVARRHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIRQONLLDPDTAVLKICDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
DB 181 DIRQONLLDPDTAVLKICDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVOLVETIKVLGTPTRREQIRENNPNYTEKFPQIKANP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVOLVETIKVLGTPTRREQIRENNPNYTEKFPQIKANP 300
QY 311 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLEACAHSPFDELNDPNVKGHPNGRDTPALF 370
DB 301 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLEACAHSPFDELNDPNVKGHPNGRDTPALF 360
QY 371 NFTQELSSNPPLATITILIPHARI 394
DB 361 NFTQELSSNPPLATITILIPHARI 384

RESULT 10
US-10-840-060-257
Sequence 257, Application US/10840060
Publication No. US20050227243A1
GENERAL INFORMATION:
APPLICANT: Cyclacel Limited
APPLICANT: Deak, Peter
APPLICANT: Frenz, Lisa
APPLICANT: Glover, David
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: 10069/2012
CURRENT APPLICATION NUMBER: US/10/840,060

CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: PCT/GB02/04780
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 0126506.5
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: GB 0128384.5
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: GB 0203185.4
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PatentIn version 3.1
SEQ ID NO 257
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-840-060-257

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2,6e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKDGSKTTVVATPGQGPDRQEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKDGSKTTVVATPGQGPDRQEVSYDTK 60
QY 71 VIGNGSGVYVQAALCDSGELVAIKVLODKRFKRELOIRKIDHCNIIVLRFFYS5G 130
DB 61 VIGNGSGVYVQAALCDSGELVAIKVLODKRFKRELOIRKIDHCNIIVLRFFYS5G 120
QY 131 EKQDEVYLVNLDVVPETVVRVARRHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKQDEVYLVNLDVVPETVVRVARRHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIRQONLLDPDTAVLKICDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
DB 181 DIRQONLLDPDTAVLKICDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVOLVETIKVLGTPTRREQIRENNPNYTEKFPQIKANP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVOLVETIKVLGTPTRREQIRENNPNYTEKFPQIKANP 300
QY 311 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLEACAHSPFDELNDPNVKGHPNGRDTPALF 370
DB 301 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLEACAHSPFDELNDPNVKGHPNGRDTPALF 360
QY 371 NFTQELSSNPPLATITILIPHARI 394
DB 361 NFTQELSSNPPLATITILIPHARI 384

RESULT 11
US-10-746-545-31
Sequence 31, Application US/10746545
Publication No. US20040171075A1
GENERAL INFORMATION:
APPLICANT: Deciphera Pharmaceuticals, Inc.
APPLICANT: Flynn, Daniel L
APPLICANT: Pettillo, Peter A
TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
FILE REFERENCE: 34475
CURRENT APPLICATION NUMBER: US/10/746,545
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: US 60/437,487
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-746-545-31

Query Match 96.7%; Score 2013; DB 4; Length 414;

Best Local Similarity 99.7%; Pred. No. 2,3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQOPSAFSGSMKVS RDKSGSKVTYVATPGQGPDRPOEVS YTDTK 70
Db 1 MSGRPRTTSPAESCKPVQOPSAFSGSMKVS RDKSGSKVTYVATPGQGPDRPOEVS YTDTK 60

Qy 71 VINGSGGVVYQALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHCNIYLRFFYS SG 130
Db 61 VINGSGGVVYQALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHCNIYLRFFYS SG 120

Qy 131 EKDEVLNLVLDVPEPTVYVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 190
Db 121 EKDEVLNLVLDVPEPTVYVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 180

Qy 191 DIKQNLILDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
Db 121 EKDEVLNLVLDVPEPTVYVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 180

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 12
US-10-278-759-6
; Sequence 6, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Malah, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237,70020,US
; CURRENT APPLICATION NUMBER: US/10/278, 759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-278-759-6

Query Match 96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2,3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 300

Qy 311 WTKVFRRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 13
US-10-135-255-1
; Sequence 1, Application US/10135255
; Publication No. US20030125332A1
; GENERAL INFORMATION:
; APPLICANT: TER HAAR, ERNST
; APPLICANT: SWENSON, LOYORKA
; APPLICANT: GREEN, JEREMY
; APPLICANT: ARNOST, MICHAEL J.
; TITLE OF INVENTION: INHIBITORS OF GSK-3 AND CRYSTAL STRUCTURES OF GSK-3B
; TITLE OF INVENTION: PROTEIN AND PROTEIN COMPLEXES
; FILE REFERENCE: VPI/01-02
; CURRENT APPLICATION NUMBER: US/10/135,255
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/361,899
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/297,094
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/287,366
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-255-1

Query Match 96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2,3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQOPSAFSGSMKVS RDKSGSKVTYVATPGQGPDRPOEVS YTDTK 70
Db 1 MSGRPRTTSPAESCKPVQOPSAFSGSMKVS RDKSGSKVTYVATPGQGPDRPOEVS YTDTK 60

Qy 71 VINGSGGVVYQALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHCNIYLRFFYS SG 130
Db 61 VINGSGGVVYQALCDSGELVAIKKYLQDKRFKNRELQIMRKLDHCNIYLRFFYS SG 120

Qy 131 EKDEVLNLVLDVPEPTVYVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 190
Db 121 EKDEVLNLVLDVPEPTVYVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 180

Qy 191 DIKQNLILDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
Db 181 DIKQNLILDPDPAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 240

Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 300

Qy 311 WTKVFRRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

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RESULT 14
US-10-746-545-15
; Sequence 15, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphera Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-545-15

Query Match          96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRITTSFAESCKPVQPSAFGSMKYSRDKSGSKTTVVATPGQGPDRQEVSYTDTK 70
DB 1 MSGRPRITTSFAESCKPVQPSAFGSMKYSRDKSGSKTTVVATPGQGPDRQEVSYTDTK 60
QY 71 VINGSGFGVYVQAKLCSGSELVAIKVLODKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 130
DB 61 VINGSGFGVYVQAKLCSGSELVAIKVLODKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 120
QY 131 EKKDEVYLNVLVDVPEVTVVVARHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKKDEVYLNVLVDVPEVTVVVARHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIKQNLILDPTAVLKLCDFGSAKQLVRGEPNYSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQNLILDPTAVLKLCDFGSAKQLVRGEPNYSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSACCVLAELLIGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLIGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPEBALALCSRLLEYTPATLTPLECAHSFPDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEBALALCSRLLEYTPATLTPLECAHSFPDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 15
US-10-746-545-18
; Sequence 18, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphera Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 18
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-545-18

Query Match          96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRITTSFAESCKPVQPSAFGSMKYSRDKSGSKTTVVATPGQGPDRQEVSYTDTK 70
DB 1 MSGRPRITTSFAESCKPVQPSAFGSMKYSRDKSGSKTTVVATPGQGPDRQEVSYTDTK 60
QY 71 VINGSGFGVYVQAKLCSGSELVAIKVLODKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 130
DB 61 VINGSGFGVYVQAKLCSGSELVAIKVLODKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 120
QY 131 EKKDEVYLNVLVDVPEVTVVVARHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKKDEVYLNVLVDVPEVTVVVARHYSRAKOTLPVIYKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIKQNLILDPTAVLKLCDFGSAKQLVRGEPNYSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKQNLILDPTAVLKLCDFGSAKQLVRGEPNYSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSACCVLAELLIGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLIGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPEBALALCSRLLEYTPATLTPLECAHSFPDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEBALALCSRLLEYTPATLTPLECAHSFPDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:22:07 ; Search time 28 Seconds
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660.637 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081
Sequence: 1 MEWPMGCGMGSGRPTTSF.....OELSNPLATILIPPHARI 394

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Gapop 10.0, Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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 - 2: /SIDSS/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
 - 3: /SIDSS/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
 - 4: /SIDSS/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
 - 5: /SIDSS/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
 - 6: /SIDSS/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
 - 7: /SIDSS/ptodata/2/pubppaa/US10_NEW_PUB.pep1.*
 - 8: /SIDSS/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
 - 9: /SIDSS/ptodata/2/pubppaa/US11_NEW_PUB.pep1.*
 - 10: /SIDSS/ptodata/2/pubppaa/US11_NEW_PUB.pep1.*
 - 11: /SIDSS/ptodata/2/pubppaa/US11_NEW_PUB.pep1.*
 - 12: /SIDSS/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------------------|---------------------|
| 1 | 2081 | 100.0 | 394 | 8 US-10-733-816-2 | Sequence 2, Appl1 |
| 2 | 2024 | 97.3 | 420 | 8 US-10-733-816-1 | Sequence 172, Appl1 |
| 3 | 2024 | 97.3 | 420 | 11 US-11-288-493-72 | Sequence 65, Appl1 |
| 4 | 1996.5 | 95.9 | 433 | 9 US-10-770-726-65 | Sequence 3, Appl1 |
| 5 | 1883.5 | 90.5 | 361 | 8 US-10-733-816-3 | Sequence 5, Appl1 |
| 6 | 1609 | 77.3 | 447 | 8 US-10-733-816-5 | Sequence 4, Appl1 |
| 7 | 1609 | 77.3 | 483 | 8 US-10-733-816-4 | Sequence 12, Appl1 |
| 8 | 1609 | 77.3 | 483 | 9 US-10-451-375-12 | Sequence 7, Appl1 |
| 9 | 1588 | 76.3 | 351 | 8 US-10-733-816-7 | Sequence 6, Appl1 |
| 10 | 1588 | 76.3 | 387 | 8 US-10-733-816-6 | Sequence 2916, Ap |
| 11 | 1296 | 62.3 | 409 | 11 US-11-188-298-2916 | Sequence 13661, A |
| 12 | 1274 | 61.2 | 414 | 11 US-11-188-298-13961 | Sequence 20391, A |
| 13 | 1264 | 60.7 | 394 | 11 US-11-188-298-20391 | Sequence 2343, Ap |
| 14 | 1259 | 60.5 | 412 | 11 US-11-188-298-2343 | Sequence 18419, A |
| 15 | 1256 | 60.4 | 411 | 11 US-11-188-298-18419 | Sequence 11847, A |
| 16 | 1256 | 60.4 | 412 | 11 US-11-188-298-11847 | Sequence 9056, Ap |
| 17 | 1255.5 | 60.3 | 405 | 11 US-11-188-298-9056 | Sequence 17827, Ap |
| 18 | 1250 | 60.1 | 407 | 11 US-11-188-298-17827 | Sequence 19883, A |
| 19 | 1250 | 60.1 | 407 | 11 US-11-188-298-19883 | Sequence 9267, Ap |
| 20 | 1249 | 60.0 | 403 | 11 US-11-188-298-9267 | Sequence 13637, A |
| 21 | 1249 | 60.0 | 403 | 11 US-11-188-298-13637 | |

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| 22 | 1248.5 | 60.0 | 412 | 11 US-11-188-298-10609 | Sequence 10609, A |
| 23 | 1244 | 59.8 | 411 | 11 US-11-188-298-10624 | Sequence 10624, A |
| 24 | 1243.5 | 59.8 | 412 | 11 US-11-188-298-3285 | Sequence 3285, Ap |
| 25 | 1243.5 | 59.7 | 419 | 11 US-11-188-298-22443 | Sequence 22443, A |
| 26 | 1241 | 59.6 | 402 | 11 US-11-188-298-15005 | Sequence 15005, A |
| 27 | 1240.5 | 59.6 | 496 | 11 US-11-188-298-14293 | Sequence 14293, A |
| 28 | 1239 | 59.5 | 409 | 11 US-11-188-298-12421 | Sequence 12421, A |
| 29 | 1235.5 | 59.4 | 400 | 11 US-11-188-298-15000 | Sequence 15000, A |
| 30 | 1234.5 | 59.3 | 404 | 11 US-11-188-298-1871 | Sequence 1871, Ap |
| 31 | 1232.5 | 59.2 | 394 | 11 US-11-188-298-22436 | Sequence 22436, A |
| 32 | 1232.5 | 59.2 | 406 | 11 US-11-188-298-4509 | Sequence 4509, Ap |
| 33 | 1232 | 59.2 | 407 | 11 US-11-188-298-464 | Sequence 464, App |
| 34 | 1231.5 | 59.2 | 397 | 11 US-11-188-298-1451 | Sequence 1451, A |
| 35 | 1230.5 | 59.1 | 403 | 11 US-11-188-298-5432 | Sequence 5432, Ap |
| 36 | 1228.5 | 59.0 | 403 | 11 US-11-188-298-21943 | Sequence 21943, A |
| 37 | 1226 | 58.9 | 411 | 11 US-11-188-298-1737 | Sequence 1737, Ap |
| 38 | 1226 | 58.9 | 468 | 11 US-11-188-298-14237 | Sequence 14237, A |
| 39 | 1225 | 58.9 | 414 | 11 US-11-188-298-17137 | Sequence 17137, A |
| 40 | 1222.5 | 58.7 | 394 | 11 US-11-188-298-2187 | Sequence 2187, Ap |
| 41 | 1222.5 | 58.7 | 401 | 11 US-11-188-298-11664 | Sequence 11664, A |
| 42 | 1220.5 | 58.6 | 341 | 11 US-11-188-298-18416 | Sequence 18416, A |
| 43 | 1218.5 | 58.6 | 421 | 11 US-11-188-298-7320 | Sequence 7320, Ap |
| 44 | 1208.5 | 58.1 | 420 | 11 US-11-188-298-10248 | Sequence 10248, A |
| 45 | 1199.5 | 57.6 | 468 | 11 US-11-188-298-17561 | Sequence 17561, A |

ALIGNMENTS

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RESULT 1
US-10-733-816-2
; Sequence 2, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT FILING DATE: US/10/733, 816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211, 412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916, 109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-2
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Best Local Similarity 100.0%; Pred. No. 3e-171;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 PQVSYTDTKYTGSGGCVYQATLCSGELVAIKKYLQDRFKRRELQIRKLDHCNIV 120
DB 61 PQVSYTDTKYTGSGGCVYQATLCSGELVAIKKYLQDRFKRRELQIRKLDHCNIV 120
QY 61 PQVSYTDTKYTGSGGCVYQATLCSGELVAIKKYLQDRFKRRELQIRKLDHCNIV 120
DB 61 PQVSYTDTKYTGSGGCVYQATLCSGELVAIKKYLQDRFKRRELQIRKLDHCNIV 120
QY 121 RLRFFSSGGEKQEVYLVLDVVPETVYRVAHYSRAKOTLPIVYVKLYMYOLFSLA 180
DB 121 RLRFFSSGGEKQEVYLVLDVVPETVYRVAHYSRAKOTLPIVYVKLYMYOLFSLA 180
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DB 181 YHSFG:CHRDIKPONLLDPDTAVLKCDFGSAKOLVRGEPNYSICRYRABELIFG 240
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DB 241 ATDYTSSIDVWSAGCVLAELLGGPIFGDSGVQDLVEIIVKLGTPTRREQIRENNPNYTE 300
QY 301 FKFPQIRAHFWTKYFRPRTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
DB 301 FKFPQIRAHFWTKYFRPRTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALFNTTOELSSNPPLATITILIPPHARI 394
DB 361 PNGRDTPALFNTTOELSSNPPLATITILIPPHARI 394

RESULT 2
US-10-733-816-1
; Sequence 1, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacela, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733.816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211.412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916.109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-1

Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 371 NPTTOELSSNPPLATITILIPPHARI 394
DB 361 NPTTOELSSNPPLATITILIPPHARI 384

RESULT 3
US-11-288-493-72
; Sequence 72, Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MPI03-015PIRMONIM
; CURRENT APPLICATION NUMBER: US/11/288.493
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772.636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-288-493-72

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Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 WSAGCVLAEILLGQPIFGDSGVQDLVEIILKVLGTPTEBOIREKMPNTEFEKPOIKAH 300
Qy 311 WTKVRPRTPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPNVXHPGRDTPALF 370
Db 301 WTKVRPRTPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPNVXHPGRDTPALF 360
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Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 4
US-10-770-726-65
; Sequence 65, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM:01079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-65

Query Match 95.9%; Score 1996.5; DB 9; Length 433;
Best Local Similarity 96.5%; Pred. No. 6.3e-164;
Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

Qy 11 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKDSKTTTVAATPGQGPDRPOEVSYTQK 70
Db 1 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKDSKTTTVAATPGQGPDRPOEVSYTQK 60
Qy 71 VINGSPGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIIVLRYPFYSSG 130
Db 61 VINGSPGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIIVLRYPFYSSG 120
Qy 131 EKKDEVYINLVLDYVPEVTVYRVAHYSAKQTLPIYVYKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKKDEVYINLVLDYVPEVTVYRVAHYSAKQTLPIYVYKLYMYQLFRSLAYIHSFGICHR 180
Qy 191 DIKPNLLDPDTAVLKLCDPESAKQVLRGEPNVSICRRYRABELFGATDNTSSIDV 250
Db 181 DIKPNLLDPDTAVLKLCDPESAKQVLRGEPNVSICRRYRABELFGATDNTSSIDV 240
Qy 251 WSAGCVLAEILLGQPIFGDSGVQDLVEIILKVLGTPTEBOIREKMPNTEFEKPOIKAH 310
Db 241 WSAGCVLAEILLGQPIFGDSGVQDLVEIILKVLGTPTEBOIREKMPNTEFEKPOIKAH 300
Qy 311 WTK-----VRRPRTPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPN 357
Db 301 WTKSSSGTGHFTSGVVRPRPPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPN 360
Qy 358 VKHPNGRDTPALFNTTOELSSNPPLATILIPPHARI 394
Db 361 VKLPNGRDTPALFNTTOELSSNPPLATILIPPHARI 397

RESULT 5
US-10-733-816-3
; Sequence 3, Application US/10733816
; Publication No. US20060088932A1
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; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-3

Query Match 90.5%; Score 1883.5; DB 8; Length 361;
Best Local Similarity 91.6%; Pred. No. 2.6e-154;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 MEYPMEEGSGMRPRTTSPAESCKPVOQPSAFSGMKVSRDKDSKTTTVAATPGQGPDR 60
Db 1 MEYPMEEGSG-----GSKTTTVAATPGQGPDR 27
Qy 61 POEVSYTDTKVINGSPGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIIV 120
Db 28 POEVSYTDTKVINGSPGVVYQAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIIV 87
Qy 121 RLRYFFSYSGEKDEVYINLVLDYVPEVTVYRVAHYSAKQTLPIYVYKLYMYQLFRSLA 180
Db 88 RLRYFFSYSGEKDEVYINLVLDYVPEVTVYRVAHYSAKQTLPIYVYKLYMYQLFRSLA 147
Qy 181 YIHSFGICHRDIKPNLLDPDTAVLKLCDPESAKQVLRGEPNVSICRRYRABELFG 240
Db 148 YIHSFGICHRDIKPNLLDPDTAVLKLCDPESAKQVLRGEPNVSICRRYRABELFG 207
Qy 241 ATDNTSSIDVWSAGCVLAEILLGQPIFGDSGVQDLVEIILKVLGTPTEBOIREKMPNTE 300
Db 208 ATDNTSSIDVWSAGCVLAEILLGQPIFGDSGVQDLVEIILKVLGTPTEBOIREKMPNTE 267
Qy 301 EKFPOIKAHPTKVFRRPRTPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPNVX 360
Db 268 EKFPOIKAHPTKVFRRPRTPEPAIALCSRLLEYTPARLTPEACAHSPFDELBDPNVX 327
Qy 361 PNGRDTPALFNTTOELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTOELSSNPPLATILIPPHARI 361

RESULT 6
US-10-733-816-5
; Sequence 5, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
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Db 180 YSSGKQKQELVLTLEVPETVVAHFTKAKLTITILYKVMYQLFRSLAYHSQG 239
Qy 187 ICHRDIKQNLDDPTAVLKLCDGSAKQVKGEPNYSICSRYYRAPELIFGATDYS 246
Db 240 VCHRIKQNLVDPDTAVLKLCDGSAKQVKGEPNYSICSRYYRAPELIFGATDYS 299
Qy 247 SIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGTPTREOIRENNPNTFEKFPQI 306
Db 300 SIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGTPTREOIRENNPNTFEKFPQI 359
Qy 307 KAHPTKVFRRPTPEALALCSRLLEYTPALTPLEACAHSPFDELDPVKGHPGRDT 366
Db 360 KAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEACAHSPFDELCLGTQLPNNRPL 419
Qy 367 PALFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAIILIPPHLR 446
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RESULT 9

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US-10-733-816-7
; Sequence 7, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Caccia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-7
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Query Match 76.3%; Score 1588; DB 8; Length 351;

Best Local Similarity 86.2%; Pred. No. 6.7e-129; Indels 0; Gaps 0;

Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

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Db 3 KTTTVAATPGGPRPOEVSITDTKVIKNGSGVGVYQAKLCDSEGLVAIKKVLQDKRKN 62
Qy 106 RELQIMKLDHCNIVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAHRSRAKQTLPIV 165
Db 63 RELQIMKLDHCNIVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAHRSRAKQTLPI 122
Qy 166 IYKLVYMYQLFRSLAYHSFGICHRDIKPNLVDPTAVLKLCDGSAKQVKGEPNVS 225
Db 123 IYKLVYMYQLFRSLAYHSFGICHRDIKPNLVDPTAVLKLCDGSAKQVKGEPNVS 182
Qy 226 YICGRYRAPPELIFGATDYSIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGT 285
Db 183 YICGRYRAPPELIFGATDYSIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGT 242
Qy 286 PTRQIRENNPNTFEKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPALTPLEAC 345
Db 243 PTRQIRENNPNTFEKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEAC 302
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Qy 346 AHSFDELDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 303 AHSFDELCLGTQLPNNRPLPPLFNFSAGELSIQPSLNAIILIPPHLR 350
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RESULT 10

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US-10-733-816-6
; Sequence 6, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Caccia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-6
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Query Match 76.3%; Score 1588; DB 8; Length 387;

Best Local Similarity 86.2%; Pred. No. 7.6e-129; Indels 0; Gaps 0;

Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

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Qy 46 KTTTVAATPGGPRPOEVSITDTKVIKNGSGVGVYQAKLCDSEGLVAIKKVLQDKRKN 105
Db 3 KTTTVAATPGGPRPOEVSITDTKVIKNGSGVGVYQAKLCDSEGLVAIKKVLQDKRKN 62
Qy 106 RELQIMKLDHCNIVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAHRSRAKQTLPIV 165
Db 63 RELQIMKLDHCNIVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAHRSRAKQTLPI 122
Qy 166 IYKLVYMYQLFRSLAYHSFGICHRDIKPNLVDPTAVLKLCDGSAKQVKGEPNVS 225
Db 123 IYKLVYMYQLFRSLAYHSFGICHRDIKPNLVDPTAVLKLCDGSAKQVKGEPNVS 182
Qy 226 YICGRYRAPPELIFGATDYSIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGT 285
Db 183 YICGRYRAPPELIFGATDYSIDWSAGCVLAELLGGPIFGDSGVQVLEIIVLGT 242
Qy 286 PTRQIRENNPNTFEKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPALTPLEAC 345
Db 243 PTRQIRENNPNTFEKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEAC 302
Qy 346 AHSFDELDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 303 AHSFDELCLGTQLPNNRPLPPLFNFSAGELSIQPSLNAIILIPPHLR 350
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RESULT 11

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US-11-188-298-2916
; Sequence 2916, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; PRIOR FILING DATE: 2005-07-22
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; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2916
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Pecunia x hybrida
US-11-188-298-2916

Query Match      62.3%; Score 1296; DB 11; Length 409;
Best Local Similarity 62.3%; Pred. No. 1.1e-103;
Matches 254; Conservative 49; Mismatches 75; Indels 30; Gaps 7;

Qy      4 MPMGGGMSGRPRTPFAESCKPVOQPSAFGSMKVSRLK-----DSK----- 46
Db      6 MPMG-----GKRTDAMLV-----KLPEINEMKTRDDKAEKEBAVVDGNGTEKGHIT 57

Qy      47 VTTVATPGQPDPRPOEVSYTDRTVINGSGFVVYQAKLDSGELVAIKVLDKRFKPR 106
Db      58 VTTI---GKKGEBKQITISWAERVGGSGFVQAKLETGETVAIKVLDKRYKPR 114

Qy      107 ELQIMRKLDHCNIVRLKRYFFSSGEEKDEVTLNVLVDYVPEYTVRVARHYSRAKQTLFVI 166
Db      115 ELQITRLLDHPNVVALRHCFPSTTE-KDELYLNLVLEVPETVYRVLRHYSKAKQOMPMI 173

Qy      167 YVKLYMYQLFRSLAYIHSFGICHRDIKQNLILDPDTAVLKLDGFGSAKOLVRGEPNVSY 226
Db      174 YVKLYTYQIFRALYIHGIGVCHRDIKQNLVLPHTQOLKLDGFGSAKVLVKEPNISY 233

Qy      227 ICSRYRABELIFGATDYTSIDVWSAGCVLAELLGQPIPGDSGVQDLVEIIKVLGTP 286
Db      234 ICSRYRABELIFGATEYTFALDIWSVGCYLAELLGQPLPGSGVQDLVEIIKVLGTP 293

Qy      287 TREQIRENNPVYTERKFPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACA 346
Db      294 TREIRKSNPNVYTERKFPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACA 353

Qy      347 HSFPELDRDPVVKHPNGRDPALFNFTQEL-SSNPLATILIPPHAR 393
Db      354 HFPDELDRDPKTRLPNGRPLPLFNFRPELKGASADILNLKILPEHAK 401

RESULT 12
US-11-188-298-13961
; Sequence 13961, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13961
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-188-298-13961

Query Match      61.2%; Score 1274; DB 11; Length 414;
Best Local Similarity 60.8%; Pred. No. 8.6e-102;
Matches 239; Conservative 63; Mismatches 81; Indels 10; Gaps 4;

Qy      8 GGGGSG-----RRTTSFAESCKPVOQPSAFGSMKVSRLDQSGSKVTTVATPGQPDPR 61
Db      12 GGGGAADPMQVDQGRSAAAAAVALPAGKKGASLMESDPTVGHIIISTTIG--GKNEBK 69

Qy      62 QEVSYTDRTVINGSGFVVYQAKLDSGELVAIKVLDKRFKQRELOIMRKLDHCNIVR 121
Db      70 RTISYMERVVGTSFGIVFQAKLETGETVAIKKVLQDKRYKRELOIMKSMHCHVVS 129

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Qy      122 LRYFFYSSGEEKDEVTLNVLVDYVPEYTVRVARHYSRAKQTLFVIYVKLYMYQLFRSLAY 181
Db      130 LKICFFST-ISRDELFLNLVMEFVPSLVVLGHYSNMQRMLLIVKLVYQIFRGLAY 188

Qy      182 IHSF-GICHRDIKQNLILDPDTAVLKLDGFGSAKOLVRGEPNVSYICSRYRABELIFG 240
Db      189 IHTVPGVCHRDVPRQNLVLDPLTHOVKICDFGSAKMLVKEGANISYICSRYRABELIFG 248

Qy      241 ATDVTSSIDVWSAGCVLAELLGQPIPGDSGVQDLVEIIKVLGTPFREQIRENNPVYTE 300
Db      249 ATETVTSSIDVWSAGCVLAELLGQPLPGSADVQDLVEIIKVLGTPFREIRMMNPVYTE 308

Qy      301 KFPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACAHSFPELDRDPVVKH 360
Db      309 FRPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACAHSFPELDRDPVVKH 368

Qy      361 PNGRDPALFNFTQELSSNPLATILIPPHAR 393
Db      369 PNGRFPPLFNFRPELKGASADILNLKILPEHAR 401

RESULT 13
US-11-188-298-20391
; Sequence 20391, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20391
; LENGTH: 394
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-20391

Query Match      60.7%; Score 1264; DB 11; Length 394;
Best Local Similarity 70.8%; Pred. No. 5.8e-101;
Matches 240; Conservative 41; Mismatches 50; Indels 8; Gaps 3;

Qy      62 QEVSYTDRTVINGSGFVVYQAKLDSGELVAIKVLDKRFKQRELOIMRKLDHCNIVR 121
Db      31 KEIQYSSCKIVGSGFVVYQAKLDSGELVAIKVLDKRFKQRELOIMRKLDHCNIVR 90

Qy      122 LRYFFYSSGEEKDEVTLNVLVDYVPEYTVRVARHYSRAKQTLFVIYVKLYMYQLFRSLAY 181
Db      91 LKAFYNSNGRQDEVTLNVLVDYVPEYTVRASHYFVKLKTMTMELVKLYIYQLFRSLAY 150

Qy      182 IHSF-GICHRDIKQNLILDPDTAVLKLDGFGSAKOLVRGEPNVSYICSRYRABELIFGA 241
Db      151 IHSQGICHRDIKQNLILDPDTATGILKLDGFGSAKILVMEPNVSYICSRYRABELIFGA 210

Qy      242 TDVTSSIDVWSAGCVLAELLGQPIPGDSGVQDLVEIIKVLGTPFREQIRENNPVYTE 301
Db      211 TNYTTKIDVWSTCVNAELMLGQPLPGSGIDQDLVEIIKVLGTPFREQIRTNPNVMEH 270

Qy      302 KFPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACAHSFPELDRDPVVK-- 359
Db      271 KFPQIKAHMPTKVFRRPTPEALALCSRLLETPTARLPLEACAHSFPELDRDPVVKLP 329

Qy      360 ---HPNG--BDTPALFNFTQELSSNPLATILIPPHAR 393
Db      330 DSRHPNGAARDLPNLDFDSRHELSIAFSMNSRLVPHSR 368

RESULT 14
US-11-188-298-2343
; Sequence 2343, Application US/11188298
; Publication No. US20060075522A1

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; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2343
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Zea mays
US-11-188-298-2343

Query Match          60.5%; Score 1259; DB 11; Length 412;
Best Local Similarity 59.5%; Pred. No. 1,7e+100;
Matches 244; Conservative 62; Mismatches 76; Indels 28; Gaps 8;

Qy 1 MEYMEGGGMSGRRTTSFASCKPVQ-----QPSAGSMKVSNDK-----DGSKVT 48
Db 1 MAAMP---GGAHG-----AGADPMQVDQPLPPAAGTAHAPADAKGAGSMIGSDPV 50

Qy 49 T--VVAATP--GCGPDRPOEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFX 104
Db 51 TGHISTITGGKNGEPKKTISTMARVVGTSFGIVFOAKCLFGETVAIKKVLQDKRFX 110

Qy 105 NRELIQMKLDHCNIVRLRYFFYSSEKKEDEVYLVLDVYBETVYRVARHYSRAKQTLF 164
Db 111 NRELIQMSMDHCNVSLKHCFFST--TSRDELFLVMEFVESLYRVLKHYSNQRMNP 169

Qy 165 VIYKLVYVQQLPRLALYHSF-GICHRDIKPNLLDPTAVLKLCDFSAGAKLVGSEPN 223
Db 170 LIIYVLYTYQILFRLAYLHIVPGVCHRDVCPQNLVDPQLHQVKICDFGSAMLVGSEAN 229

Qy 224 VSYICSRYYRAPELIFGATDYSIDVWSAGCVLAELLLGQPIFPDGSVDQVLEIIRKL 283
Db 230 ISYICSRYYRAPELIFGATEYTSIDISAGCVLAELLLGQPLFPGESVDQVLEIIRKL 289

Qy 284 GTPREQIRENNPNYTEFKEPQIKAPMTKVFRPRTPEAIALCSRLEYPPTARLTPLE 343
Db 290 GTPREIRICNNPNYTEFRFPQIKAPMHKIFHKMPPEAIDLASRLQYSPNLRCTALE 349

Qy 344 ACAHSFPELADPNVKNHNGRDTPALFNFPTQELSSNPPLATILIPPHAR 393
Db 350 ACAHFFPELBRPHARLPNGRFPPLFNFKQELANASPELINRLIPDHAR 399

RESULT 15
US-11-188-298-18419
; Sequence 18419, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18419
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Medicago sativa
US-11-188-298-18419

Query Match          60.4%; Score 1256; DB 11; Length 411;
Best Local Similarity 61.2%; Pred. No. 3e+100;
Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

Qy 6 MEGGMSGRPRTTSFASCKPV---QPSAGSMKVSNDK-----DGSKVT---VV 51
Db 6 MEGGMSGRPRTTSFASCKPV---QPSAGSMKVSNDK-----DGSKVT---VV 51
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Db 1 MASGVA--PASGFIDKNASSVGEKLPENMDMKIRDDKEMEATYIVDNGTGTGHIIV 58
Qy 52 ATPGGPRP--QBSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFXREIQT 110
Db 59 TTIGKNGQPKQTISTMARVVGTSFGIVFOAKCLFGETVAIKKVLQDKRFXREIQT 118
Qy 111 MRKLDHCNIVRLRYFFYSSEKKEDEVYLVLDVYBETVYRVARHYSRAKQTLFPIYVYL 170
Db 119 MKLDHNPVSLKHCFFSTTE--KDELYLVNLEIVPEVSKYIRHYNKQRMNPPIYVYL 177

Qy 171 YMYQLFRSLAYIH-SFGICHRDIKPNLLDPTAVLKLCDFSAGAKLVGSEPNVSYICS 229
Db 178 YSYQICRALAYIHNSIGVCHRDVCPQNLVDPQLHQVKICDFGSAMLVGSEPNVSYICS 237

Qy 230 RYRAPPELIFGATDYSIDVWSAGCVLAELLLGQPIFPDGSVDQVLEIIRKLGTPTRE 289
Db 238 RYRAPPELIFGATEYTSIDISAGCVLELLGQPLFPGESVDQVLEIIRKLGTPTRE 297

Qy 290 QIRENNPNYTEFKEPQIKAPMTKVFRPRTPEAIALCSRLEYPPTARLTPLEACAHSF 349
Db 298 EIKCNPVYTEFKEPQIKAPMHKIFHKMPPEAIDLASRLQYSPNLRCTALEALVHPF 357

Qy 350 FDELADPNVKNHNGRDTPALFNFPTQELSSNP-PLATILIPPHAR 393
Db 358 YDVRDPVTRLPNGRFLPPLFNFKNELKGVPAEWLVLTVEPPHAR 402

Search completed: May 16, 2006, 15:25:20
Job time : 29 secs
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